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February 12,

2004,

01:54:29 ; Search time 615.146 Seconds (without alignments)
1396.582 Million cell updates/sec

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GenCore version (c) 1993 - 2004

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em\_htg\_wam::\*
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score greater than or equal to the score of the result being and is derived by analysis of the total score distribution. printed,

SUMMARIES

## REFERENCE AUTHORS TITLE . VERSION KEYWORDS SOURCE ORGANISM RESULT 1 AX350501 LOCUS DEFINITION ACCESSION Regult No. იი JOURNAL Score AX350501 Sequence 13 AX350501 AX350501.1 Homo Liggett, S.B. and Small, K.M. Alpha-2 adrenergic receptor polymorphisms Patent: WO 0179561-A 13 25-OCT-2001; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo sapiens Query Match sapiens Length from GI:18616097 (human) 21 bp Patent WO0179561. BB 99 $\sigma\sigma\sigma\sigma\sigma\sigma\sigma$ 4 4 4 6 0 6 0 6 0 010444400 44444 40 ARU427256 APA419813 EAT419810 PCA427417 AF337543 AF337542 LAL335940 MM0427255 SVU315942 BPH251175 BTAAR28 AF3AR28 AF3AR28 AF3AR29 AF3AR39 AF3AR39 AX350501 AF337537 RAM315937 CSP251181 MLA251107 FCA251174 AF337538 NAL419805 RCR419806 PVI251176 PVI251176 DDAAR28 DDAAR28 TMA2511109 CVA251182 AX350489 AR270618 HUMADRA2RA AX548756 AX344977 AX348498 AF005900 ij ALIGNMENTS DNA linear AJ419806 Rhinoloph AJ251176 Phoca vit AP337543 Taphozous Y15947 Dugong dugo AJ251180 Trichechu AJ251180 Trichechu AJ251181 Cynocepha AJ419813 Antrozous AJ419813 Antrozous AJ419813 Antrozous AJ419813 Republionu AJ427417 Physeter AF337547 Tagarder AJ315940 Lagenorhy AJ427255 Marmota m AJ315942 Sciurus v AJ251175 Balaenopt Y15944 Bos taurus AJ37540 Myotis da AJ505821 Lama paco AJ251180 Macrotus AJ427259 Anomaluru AJ427259 Anomaluru AJ427259 Anomaluru AJ427259 Anomaluru AJ427259 Anomaluru AJ427259 Anomaluru AJ427251 Dipodomys AJ315941 Lama paco AJ505820 Manis tet AJ427261 Dipodomys AJ350489 Sequence AR316895 Homo sapi AX350490 Sequence AR316895 Homo sapi AX350491 Human alpha AX54877 Sequence AX344977 Sequence AX344977 Sequence AX350501 Sequence AF337539 Pteropus AJ315937 Rousettus AJ251181 Cynopteru AJ251107 Micropota AJ251174 Felis cat AJ25137538 Hipposide AJ419805 Description PAT Euteleostomi; Hipposide Nyctimene Rhinoloph 06-FEB-2002

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                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Springer, M.S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Chiroptera; Megachiroptera; Pteropodidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AJ315937.1 GI:21212918
adra2b gene; alpha 2B adrenergic receptor
Rousettus amplexicaudatus (Geoffroy's rousette)
Rousettus amplexicaudatus
Rousettus amplexicaudatus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Chiroptera; Megachiroptera; Pteropodidae;
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Resolution of the early placental mammal radiation using Bayesian
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Ryder,O.A., Stanhope,M.J.,
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AJ251107.1
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Parallel adaptive radiations in two major clades of placental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aar2B gene; alpha adrenergic receptor 2B.
cynopterus sphinx (Indian short-nosed fruit bat)
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cynopterus
  Unpublished 2 (bases 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mammals
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                                                                                                                  van Dijk, M.A.M.,
                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Insectivora; Tenrecidae; Potamogalinae;
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/protein_id="CAC15684.1"
/db_xref="Gi:1132257"
/db_xref="SPTREMBL:Q9GL20"
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RALEYNSKRTPBRIKCIILTVWLIAAVISLPPLIYKGDGGPQPHGAPQCKLNQEAWYI
LASSIGSFFAPCLIMILVYLRIYLIAKRSHRRGPRAKGGLRDSESKQPHRVPGGPSTL
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EIGEEEDECEPQALPASPASACSPPRQQPQGSRVLATLRGQVLLGKGLGTASGQWWRR
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/mol_type="genomic DNA"
/db_xref="taxon:9400"
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Pred. No. 18;
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University of Nijmegen,
                                                                                                                                                                                                                                                                                    Submitted (18-NOV-1999) University of Nijmegen,
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Direct Submission
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Mammalia; Eutheria; Carnivora; Fissipedia; Felidae;
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/db xref="GI:11191768"
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DILVATLIIPSSLANBLLGYWYFRHTWCEVYLLADVLFCTSSIVHLCAISLDRYWAVS
RALEYNSKRTPRRIKCHILTTWLIAAAISLAPPLIYKGDQPQPHGRGQCSKQPHPLAAGTS
RALEYNSKRTPACHIMILVYLRIYLIAKRSSRCRGPGSKGTSRGGVGSKQPHPLAAGTS
AKPSTITSSLAVAGBAAGQQKSTGEBGSTFXDDVAFTLPSWAAAHPHSGLCQKEGGTS
AKPSTITSSLAVAGBAAGQQWAPASPASAGSPPLQQPRGSRVLATIRGQVLLSRGLGAAGQWW
RRRTQLTREKKFTFVLAVVIGVFVLCWFPFFFSYSLGAICPQHCKVPHGLF"
76 a 411 c 339 g 230 t
/gene="aar2B"
/codon_start=2
/product="alpha adrenergic receptor 2B"
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1. .1156
                                                                                                                                                   mol_type="genomic_DN/db_xref="taxon:9685"
                                                                                                                                                                                                                                                              ocation/Qualifiers
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                                                                                                                                                                                                                organism="Felis catus"
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Pred. No.
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                                                                                                                                                                                                                                                                                                                  Madsen O., Department of P.O. box 9101, 6500 HB
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California, 1354 Speith, Riverside, CA 92521, USA
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Jong, W.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Chiroptera; Microchiroptera; Rhinolophidae;
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VSPEEAGEEDECGEPOVLPASPASACRFPLOPGSPVLPFTWPALPHAGQGPKEGVCG
GQWWRRAQLTREKRFTFVLAVVIGVFVLCWFPFFFSYSLGAICPQULKGRAGAG
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/note="A2AB"
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<1. .>1167
                                                                                                                                                                                                                                                                                         'gene="aar2B"
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/db_xref="taxon:110941"
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/db_xref="GI:11322249"
/db_xref="SPTREMBL:Q9GL17"
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LASSIGSFFAPCLIMILVYLRYYLIAAVISLPPLIYKGDQGPQPRGRPQCKLNQEAWYI
MFILASIGASGEANGHSKPTGAKEEGETPEDDATPALPSWGALPNGGQRKEGVCGA
WMRRAQLTREKGFTPALPASPASACSPPLQPPGGSRVLATLRGQVLLGRGVCTSSGQ
WMRRAQLTREKGFTFALPASPASACSPPLQPPGSRVLATLRGQVLLGRGVCTSSGQ
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Microbat paraphyly and the convergent evolution of a key innovation in Old World rhinolophoid microbats
Proc. Natl. Acad. Sci. U.S.A. 99 (3), 1431-1436 (2002)
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Madsen,O.
Direct Submission
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AJ419805.1 GI:18643971
adra2b gene; alpha 2B adrenergic receptor.
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/Codon_start=1
/product="alpha 2B adrenergic receptor"
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/db_xref="g
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                                                                                                                                   aar2B gene; alpha adrenergic receptor 2B.
Phoca vitulina (harbor seal)
Phoca vitulina
Phoca vitulina
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Carnivora; Pinnipedia; Phocidae; Phoca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Teeling, E.C., Madsen, O., Van den Bussche, R.A., de Jong, W.W., Stanhope, M.J. and Springer, M.S. Microbat paraphyly and the convergent evolution of a key innovation in Old World rhinolophoid microbats

Proc. Natl. Acad. Sci. U.S.A. 99 (3), 1431-1436 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptor.
AJ419806
AJ419806.1 GI:18643973
adra2b gene; alpha 2B adrenergic receptor.
Rhinolophus creaghi
Rhinolophus creaghi
Nature 409 (6820), 610-614 (2001) 21082081 11214318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (12-NOV-2001) Madsen O., 161 Biochemistry, U
Nijmegen, P.O. Box 9101, 6500 HB Nijmegen, NETHERLANDS
Location/Qualifiers
                                                                 Madsen,O., Scally,M., Douady,C.J., Kao,D.J., DeBry,R.W., Adki
Amrine,H.M., Stanhope,M.J., de Jong,W.W. and Springer,M.S.
Parallel adaptive radiations in two major clades of placental
                                                                                                                                                                                                                           AJ251176
AJ251176.1 GI:11322419
                                                                                                                                                                                                                                                            PVI251176
Phoca vitulina partial aar2B
                                                      mammals
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Mammalia; Eutheria; Chiroptera; Microchiroptera; Rhinolophidae;
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/protein_id="CAD11973.1"
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GQWWRRRAQLTREKRFTFVLAVVIGVFVLCWFPFFFSYSLGAICPQHCKVPHGLF"
95 a 391 c 344 g 235 t 2 others
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Best Local Similarity
Matches 21; Conser
                                                                                       Submitted (17-JAN-2001) Department of Biology, University California, 1354 Speith, Riverside, CA 92521, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission Submitted (18-NOV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (18-NOV-1999) Madsen O., Department of Biochemistry, University of Nijmegen, P.O. box 9101, 6500 HB Nijmegen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 1168)
Madsen, O.
                                                                                                                                      Direct Submission
                                                                                                                                                                                                                              Integrated fossil and molecular data reconstruct bat echolocation Proc. Natl. Acad. Sci. U.S.A. 98 (11), 6241-6246 (2001)
                                                                                                                                                                                                                                                                          Springer, M.S.,
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Mammalia; Eutheria; Chiroptera; Microchiroptera; Emballonuridae;
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ringer.M.S., Teeling,E.C.,
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                                                                                                                                                                   Stanhope, M.J.
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Direct Submission
Submitted (15-NOV-1999) O. Madsen, University of Nijmegen,
Submitted (15-NOV-1999) O. Madsen, University of Nijmegen,
Of Biochemistry, PO Box 9101, NL-6500 HB Nijmegen,
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3 (bases 1 to 1171)
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Submitted (16-DEC-1997) O. Madsen,
Department of Biochemistry, PO Box
NETHERLANDS
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Highly congruent molecular
of edemic African mammals
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alpha adrenergic receptor; subtype Dugong dugon (dugong)
Dugong dugon
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Mammalia; Eutheria; Sirenia; Dugongidae; Dugong.
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ilarity 100.0%;
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dugon gene encoding alpha
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                                                                                                                                                                                                                                                                                                                                     , 1999 this sequence version replaced gi:3288142.
Location/Qualifiers
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/product="alpha adrenergic receptor 2B"
/protein_id="AAK55308.1"
/db_xref="GI:14164938"
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/product="alpha adrenergic receptor
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Pred. No. 18;
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9101, NL-6500 HB Nijmegen,
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21; Conserv
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GCTCATCATCCCTTTCTCGCT 171
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University of Nijmegen, P.O. box 9101,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AJ251109 1 GT:11191771
aar2B gene; alpha adrenergic receptor;
Trichechus manatus (Caribbean manatee)
Trichechus manatus (Caribean manatee)
Eukaryota; Metazoa; Chordata; Craniata;
Mammalia; Eutheria; Sirenia; Trichechic
                       GCTCATCATCCCTTTCTCGCT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Madsen,O.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Probing 1the protein sequence support for the 'African clade'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NETHERLANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
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Trichechus manatus partial aar2B
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                                                                                                                                                         183
                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 1171)
                                                                                                                           /codon_start=2
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/protein_id="CAC16418.1"
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RALEXNSKRTPRRIKRILITVWLIAAAISLPDLIYKGDQFDQPRGRPQCKLNQEAWYI
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ANLFTLASSLAVAGBADGHSMPPGEKERETSEDPGTPTLPESMPVLPNSGQQCKEGVC
ANLFTLASSLAVAGBADGHSMPPGEKERETSEDPGTPTLPESMPVLLNSGQCQCKEGVC
GASLEBEADKEBEEECGPPAVPASPATACSPPLQQPGGSRVLATLRGQVFLGRGVGAA
GASLEBEADKEBEEECGPPAVPASPATACSPPLQQPGGSRVLATLRGQVFLGRGVGAA
GGQWWRRRAQLTREKETFVLAVVIGVFVLCWFPFFFSYSLGAAICPQHCRVPHGLF"
183 a 404 c 342 g 242 t
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LSSSIGSFFAPCLIMILVYLRIYLIAKRSHRRGPGAKGGPKKGESKQPHSLDSGPSAL
ANLPTLAASLAVAGEANGHSMPPGEKERETSEDFGTFTLPPSWPVLPNSGQGOKGGVC
GASLEEEADKEEEEECGFPAVPASPATACNPPLQQPOGSQVLATLRGQVFLGRGVGAA
GGQWWRRWAQLTREKRFTFVLAVVIGVFVLCWFPFFFSYSLGAICPQHCKVPHGLF"
a 397 c 337 g 247 t 1 others
                                                                                  100.0%;
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Sirenia; Trichechidae; Trichechus.
                                                                                  Score 21;
Pred. No.
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Pred. No. 18;
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101, 6500 HB Nijmegen,
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          AJ427256
AJ427256.1 GI:21655547
AJ427256.1 GI:21655547
A2AB gene; alpha 2B adrenergic receptor.
Aplodontia rufa
Aplodontia rufa
Bukeryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Aplodontidae;
Aplodontia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Madsen,O., Scally,M., Douady,C.J., Kao,D.J., DeBry,R.W., Adki
Amrine,H.M., Stanhope,M.J., de Jong,W.W. and Springer,M.S.
Parallel adaptive radiations in two major clades of placental
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aar28 gene; alpha adrenergic receptor 2B.
cynocephalus variegatus (Malayan flying lemur)
cynocephalus variegatus
cynocephalus variegatus
Eukaryota; Metazoa; Chordata; Craniata; Verteb
Mammalia; Eutheria; Dermoptera; Cynocephalidae
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Aplodontia rufa partial
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//procdingt="alpha adrenergic receptor 2B"
//procdingt="alpha adrenergic receptor 2B"
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RALEYNSKRTPRRIKCIILTVWLLAAVISLPLIYKGGOGOPQPLGREGOKSKORRPGPGGALAS
RALEYNSKRTPRRIKCIILTVWLLAAVISLPLIYKGGOGGGEGESKORRPGPGGALAS
RALPAQASPLASAGEANGOSKPTGEKEEGEISEDPGTOTLPPSWTALPNSGOGOKEGV
CGASPGEBAEBGAEBGAEPAVPVSSASICSPPLQOPGGSSVGLATLAGHVLLGRGVCGV
GGQWMRRRRAQLSREKRTFTLAVVIGAFVLCWFPFFFSYSLGAICPORCKVPHGLF"
3 a 388 c 369 g 241 t
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|mol_type="genomic DNA"
|db_xref="taxon:9457"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (04-JAN-2002) Douzery E.J.P.,
1'Evolution, Lab. Paleonto., Paleobio.,
Montpellier II, Pl. E. Bataillon, 34 099
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Douzery, E.J.P.
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/number=1
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/product="alpha 2B adrenergic receptor"
/protein_id="CAD20294.1"
/db_xref="GI:21655548"
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/mol_type="genomic DNA"
/db_xref="taxon:51342"
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Match Length
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ABX17873	AAH32040	ABK37708	ABZ43146	AAS42422	ABN89128	ABN89127	ABQ88380	ABT05663	ABK37734	ABN89119	ABN89118	AAS42448	ABL08720	ABL08624 ·	AAA76276	ABV43654	ABV34803	ABV04521	ABV13690	AAC08191	ABL18138	ABL18139	ABX83493	AAD28363	ABL32073	ABZ42623	ACA56582	AAT59499	AAQ14151	ABQ47501	ABQ47500	AAI99918	AAI99917	AAD28365	0	ABZ42624
cDNA encoding huma	Human olfactory re	DNA encoding G-cou	Human GPCR polynuc	Human cDNA encodin	Human GPCR8b nucle	Human GPCR8a nucle	Human G protein co	GPCR 12 protein en	DNA encoding G-cou		Human GPCR4a nucle		Drosophila melanog	77	thic	Human prostate exp			prostate	Human secreted pro	Drosophila melanog	Drosophila melanog	Corn ear-derived p		immune	alpha 2a-ad	signallir	alpha-2k	Human alpha 2 beta	m	Oligonucleotide fo	alpha-2AAR		Human chemically t		Human alpha 2b-adr

## ALIGNMENTS

AAI99907 standard; DNA; 21

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RESULT 1
AA19907
ID AA19
XX AA19
XX AA19
XX Huma
XX Huma
XX Huma
XX Huma
XX Homc
Cent
XX Poly
XX WO20
XX Poly
XX IIII
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PR 11-1
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Liggett SB,
                                                                                                                                                                                                                                                  17-APR-2000; 2000US-0551744
10-AUG-2000; 2000US-0636259
19-OCT-2000; 2000US-0692077
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Small KM;
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RESULT 2
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AC AADO
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AX Huma
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Best Local S
Matches 21
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                                                                                                                                                                                                                                                                  Homo
                                                                                                                                                                                                                                                                                                                                                        Human; cardiant; gene therapy; alpha2B-adrenoceptor; alpha2B-AR; glutamic acid repeat; intracellular loop; chromosome 2; catechol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAD04761 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor gene (I)-(III) by detecting a polymorphic site, co (a) obtaining a sample having a polymucleotide encoding an alpha2A or alpha2C or fragment or complement of; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for determining whether an individual is at increased risk of developing a disease associated with the corresponding receptor comprises detecting a polymorphic site -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention
                                                                                                                                                                                                                                                                sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                            alpha2B-adrenoceptor (alpha2B-AR) variant gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001-611728/70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCTCATCATCCCTTTCTCGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
llarity 100.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112; 163pp; English
                                                                                                                          /*tag= a
/product= "Human alpha2B-adrenoceptor (alpha2B-AR)
variant protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N
                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA; 1344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genotyping an by detecting a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 21;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         an alpha-2B, 2A
g a polymorphic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, or 2C
site, cc
                                                                                                                                                                                                                                                                                                                                                               catecholamine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2C adrenergic, comprising; an alpha-2B,
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WO200129082-A1

WO200179561-A2

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AAI99906
ID AAI5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is a gene encoding human alpha2B-adrenoceptor (alpha2B-AR) variant protein. Alpha2B-AR has a glutamic acid repeat celement (amino acids 298-309) of 12 glutamates, in an acidic stretch of 18 amino acids (amino acids 294-311), located in the third intracellular 1900 of the receptor polypeptide. The variant is obtained by deletion of 1900 celement is located on chromosome 2. Alpha2-AR mediate many of the 1900 celement is located on chromosome 2. Alpha2-AR mediate many of the 1900 celement is located on chromosome 2. Alpha2-AR mediate many of the 1900 celement is located on chromosome 2. Alpha2-AR mediate many of the 1900 celement in 1900 celem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                         Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor; polymorphic site; allelic variant; cardiovascular disease; central nervous system disease; adenylyl cyclase; MAP kinase activity; phosphorylation; inositol phosphate; alpha-2BAR; chromosome 2; ds.
                                                                                                                                                                                                                                                                                                                             Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human alpha-2BAR third intracellular loop variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAI99906;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAI99906 standard; DNA; 1344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1344 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New DNA molecule encoding variant specific adrenoceptor protein with deletion of specific amino acids located in the third intracellular loop of the polypeptide, for treating vascular contraction of coronary arteries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Snapir A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAE00989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-OCT-2000; 2000WO-FI00913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                               /product= "alpha-2BAR"
/note= "sequenca"
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                                                      "sequence is deleted for a 9 nucleotide polymorphic site found at nucleotides of the wildtype alpha-2BAR protein (AA)
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T, Tuomainen 7,
Valkonen V;
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Pred. No. 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             400 G;
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T, Lakka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             266 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        encoding
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Nyyssoenen
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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic CC receptor gene (I)-(III) by detecting a polymorphic site, comprising; CC (a) obtaining a sample having a polymorphic site, comprising; CC (a) postaining a sample having a polymorphic site comprising complement of; and CC (b) detecting a polymorphic site comprising nucleotide positions 901-909 CC of (I), a site comprising (A) (ggggggggcg) or (B) (gggggggtggg) at CC positions 961-972 of (III). The method may be used for genotyping an CC positions 961-972 of (III). The method may be used for genotyping an CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine CC whether an individual is at increased risk of developing a disease CC second complete which correlate to disease selected from cardiovascular CC disease, central nervous system disease selected from cardiovascular CC disease, central nervous system disease selected from cardiovascular CC disease, central nervous system disease and combinations of these. In CC combinations of these, or alpha2C agonist (e.g. epinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239, CC rauwolscine, idazoxan, tolazoline, guanabenz, UK14304, BHT933 and CC combinations of the polymorphic site and correlating the site to a predetermined response (where the response is correlated to adenylyl CC cyclase, MAP kinase activity, phosphorylation or inosito phosphate CC (Aligogos). The polymorphic site and correlated to adenylyl CC cyclase, MAP present sequence is that of the third intracellular loop of the human alpha-2BAR variant, the sequence is deleted for a 9 nucleotide CC (Aligogos).
                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 21
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10-AUG-2000;
19-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for determining whether an individual is at increased risk of developing a disease associated with the corresponding receptor comprises detecting
Human; hypertension; alpha-2B-adrenoceptor; A hypertension; hypotensive; variant; gene; ds.
                                                   Human alpha-2B-adrenoceptor variant DNA
                                                                                                                            AAD44388;
                                                                                                                                                           AAD44388 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 5; Page 144-145; 163pp; English
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SMALL K M.
                                                                                                                                                                                                                                                  GCTCATCATCCCTTTCTCGCT 209
                                                                                                                                                                                                                                                                                   GCTCATCATCCCTTTCTCGCT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; 2000US-0551744.
; 2000US-0636259.
; 2000US-0692077.
                                                                                                                                                                                                                                                                                                                    100.0%;
llarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Small KM
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                                                                                        (first
                                                                                                                                                                                                                                                                                                                                                                                           BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               site
                                                                                                                                                                                                                                                                                                                                                                                           220
                                                                                                                                                           DNA; 1344
                                                                                        entry)
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                                                                                                                                                                                                                                                                                                                                                                                           458
                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                    Score 21; DB
Pred. No. 3.2
D; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           C; 400
                                                                                                                                                                                                                                                                                                                                                                                          <u>ن</u>
                                                                                                                                                                                                                                                                                                                                      3.2
                                                                                                                                                                                                                                                                                                                                                                                          266 T; 0
                                                                                                                                                                                                                                                                                                                                                       BB
                    AR;
                                                                                                                                                                                                                                                                                                                                                       23;
                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                           other;
                                                                                                                                                                                                                                                                                                                                                       Length 1344;
                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                       0
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                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 21
                                                                                        Human; cardiant; gene therapy; alpha2B-adrenoceptor; alpha2B-AR; glutamic acid repeat; intracellular loop; chromosome 2; catechol norepinephrine; epinephrine; therapy; vascular contraction; coronary artery; coronary heat disease; CHD; chronic angina pectacute myocardial infarction; AMI; Prinzmetal's variant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a method for detecting a risk of hypertension by determining the pattern of alleles encoding a variant alpha-2B-adrenoceptor (AR) potein. The methods and compositions of the invention are useful for detecting risks and targeting treatment for hypertension. The kit is also useful for selecting for clinical drug trials testing the antihypertensive effect of compounds. The present sequence is human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detecting a risk of hypertension and targeting treatment
by determining the pattern of alleles encoding a variant
alpha-2-adrenoceptor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
Synthetic.
                                                                     Homo
                                                                                                                                                           Human
                                                                                                                                                                                   04-JUL-2001
                                                                                                                                                                                                          AAD04762;
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1344 BP;
                                                                                                                                                                                                                                                                                                                                                                                                       alpha-2B-adrenoceptor variant DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 24-26; 35pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salonen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-FEB-2001; 2001FI-0000323.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-FEB-2002; 2002WO-FI00113.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-AUG-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200266617-A1.
                                                                                                                                                                                                                               AAD04762 standard; DNA; 1353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (JURI-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2002-667063/71.
)B; AAE26633.
                                                                     sapiens
                                                                                                                                                                                                                                                                                         189
                                                                                                                                                           alpha2B-adrenoceptor (alpha2B-AR) gene
                                                                                                                                                                                                                                                                                                             س
                                                                                                                                                                                                                                                                                                                                     21;
                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                       GCTCATCATCCCTTTCTCGCT
                                                                                                                                                                                                                                                                                                              GCTCATCATCCCTTTCTCGCT 21
                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                  (first entry)
/*tag= a
/product=
protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= "Human alpha-2B-adrenoceptor variant
protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                   1..1353
                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= a
                                                                                                                                                                                                                                                                                                                                                                               219 A;
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                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                 459 C;
             "Human
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                                                                                                                                                                                                                                                                                                                                   Score 21; DB 2
Pred. No. 3.2;
0; Mismatches
                                                                                                                                                                                                                                                                                         209
                                                                                                                                                                                                                                                                                                                                                                                 400
             alpha2B-adrenoceptor
                                                                                                                                                                                                                                                                                                                                                                                 <u>و</u>
                                                                                                                                                                                                                                                                                                                                                                                 266 T; 0
                                                                                                                                                                                                                                                                                                                                                         24;
                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                  other;
                                                                                                                                                                                                                                                                                                                                                         Length 1344;
              (alpha2B-AR)
                                                                                                                          catecholamine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in
                                                                                                    pectoris;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a subject
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RESULT 6
AA19905
ID AA19
XX AA19
XX AA19
XX AA19
XX Huma
DE Huma
XX Huma
XX Huma
XX Pool
KW Pool
KW Pool
KW Pool
KW Pool
KW Gen
XX Hom
XX FH Key
FT CD:
                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
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Best Local S
Matches 21
                                                                                                    Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor; polymorphic site; allelic variant; cardiovascular disease; central nervous system disease; adenylyl cyclase; MAP kinase activity; phosphorylation; inositol phosphate; alpha-2BAR; GenBank Accession AF009500; chromosome 2; ds.
                                                                                                                                                                                  Human alpha-2BAR third intracellular loop encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is a gene encoding human alpha2B-adrenoceptor (alpha2B-AR) protein. Alpha2B-AR has a glittamic acid repeat element (amino acids 298-309) of 12 glutamates, in an acidic stretch of 18 amino the receptor polypeptide. Alpha2B-AR gene is located on chromosome 2. Alpha2-AR mediate many of the physiological effects of the catecholamines, norepinephrine and epinephrine. An antagonist of vascular contraction of coronary arteries and a disease involving as coronary heat disease (CHD), unstable chronic angina pectoris which is clinically expressed as Prinzmetal's variant form or acute myocardial infarction (AMI). Alpha2B-AR gene is used in gene therapy.
                                                                                                                                                                                                                                                                    AAI99905 standard; DNA;
                                                                                                                                                                                                                       18-FEB-2002
                                                                                                                                                                                                                                                AAI99905
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1353 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 27-29; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New DNA molecule encoding variant specific adrenoceptor protein with deletion of specific amino acids located in the third intracellular loop of the polypeptide, for treating vascular contraction of coronary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Snapir A, Ho
Scheinin M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salonen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-OCT-2000; 2000WO-FI00913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (JUVA-) JUVANTIA PHARMA
                                                                                          sapiens
                                                                                                                                                                                                                                                                                                                                          189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-300318/31.
DB; AAE00990.
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                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                         GCTCATCATCCCTTTCTCGCT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Heinonen P, Al
                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kauhanen J,
                                 /*tag=
     /product= "alpha-2BAR"
/note= "sequence includes a 9
                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0422985
                                                                                                                                                                                                                                                                                                                                                                                                                                   223 A; 459 C; 405 G; 266 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alhopuro P, Ka
IT, Tuomainen T,
I, Valkonen V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CIL
                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                  Score 21; DB
Pred. No. 3.2
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                            DB
3.2;
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                                                                                                                                                                                                                                                                                                                                                                                                          22;
nucleotide polymorphic
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                                                                                                                                                                                                                                                                                                                                                                                                        Length 1353;
                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                     DNA.
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Nyyssoenen
                                                                                                                                                                                                                                                                                                                                                                              0,
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                                                                                                                                                                                                                                                                                                                                                                              Gaps
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RESULT 7
AAD44389
ID AAD4
XX
AC AAD4
XX
DT 13-D
XX

standard;

DNA; 1353

ВP

13-DEC-2002 AAD44389; AAD44389

(first entry)

문 S

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CC The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic CC (a) obtaining a sample having a polymorphic site, comprising; CC (a) obtaining a sample having a polymorphic seconding an alpha-2B, CC (b) detecting a polymorphic site comprising mucleotide positions 901-909 (CC of (I)), a site comprising cytosine or guanine at position 753 of (IIV) (CC or a site comprising (A) (939309390ccg) or (B) (93939393ccg) at CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine CC whether an individual is at increased risk of developing at a disease control site which correlate to disease selected from cardiovascular CC disease, central nervous system disease and combinations of these. In CC disease, central nervous system disease and combinations of these. In CC combinations of these) or antagonist (e.g. epinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and CC rauwolscine, idazoxan, tolazoline, phantolamine and combinations of combinations of these) by detecting the polymorphic site and correlating the site to a CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate CC alpha-2BAR (GenBank Accession AF009500), the sequence includes CC alpha-2BAR variant (AA199906).
                                                               Query Match
Best Local S
Matches 21
                                                                                                                        Sequence 1353 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Page 144; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for determining whether an individual is at increased risk of developing a disease associated with the corresponding receptor comprises detecting a polymorphic site -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-APR-2000;
10-AUG-2000;
19-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liggett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (LIGG/)
(SMAL/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-APR-2001; 2001WO-US12575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200179561-A2.
      189
                   1 GCTCATCATCCCTTTCTCGCT
                                                               21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-611728/70
                                                                              Similarity
GCTCATCATCCCTTTCTCGCT
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SMALL K M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SB,
                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; 2000US-0551744.
; 2000US-0636259.
; 2000US-0692077.
                                                                                                                     224 A; 458
                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              at nucleotides 901-909
variant (AAI99906)"
                                                          0,
                                                                                                                   C; 405
                                                                       Score
Pred.
 209
                             21
                                                          Mismatches
                                                                                   21:
                                                                         No.
                                                                                                                   <u>ი</u>
                                                                                                                266 T; 0 other;
                                                                                    DB 23;
                                                       0,
                                                                                 Length 1353;
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                                                     Indels
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                                                    0,
                                                  Gaps
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Human

alpha-2B-adrenoceptor gene

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RESULT 8
ACAS6583
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                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method for detecting a risk of hypertension by determining the pattern of alleles encoding a variant alpha-2B-adrenoceptor (AR) protein. The methods and compositions of the invention are useful for detecting risks and targeting treatment for hypertension. The kit is also useful for selecting for clinical drug trials testing
                                                                                        Human; probe; ss; array element; Parkinson's disease; signalling pathway population; cancer; adenocarcinoma immunopathy; AIDS; asthma; neuropathy; Alzheimer's di
                                                                                                                                                                                                                                                                                                                                                                                     The kit is also useful for selecting for clinical drug
the antihypertensive effect of compounds. The present
alpha-2B-adrenoceptor gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detecting a risk of hypertension and targeting treatment in a by determining the pattern of alleles encoding a variant alpha-2-adrenoceptor -
 30-JAN-1998;
                       31-DEC-2002
                                                                                                                                     Human signalling
                                                                                                                                                               06-JUN-2003
                                                                                                                                                                                                           ACA56583 standard;
                                                                                                                                                                                                                                                                                                                                                               Sequence 1353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 27-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-FEB-2001; 2001FI-0000323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; hypertension; alpha-2B-adrenoceptor; AR; antihypertensive, hypertension; hypotensive; gene; ds.
                                                                                                                                                                                      ACA56583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-FEB-2002;
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                                                                    sapiens
                                                                                                                                                                                                                                                                     189
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                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2002WO-FI00113
                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                              BP; 223 A; 459 C; 405
98US-0016434.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product= "Human alpha-2B-adrenoceptor protein"
                                                                                                                                       pathway polynucleotide
                                                                                                                                                                                                           CDNA; 2072
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                                                                                                                                                                                                                                                                                                                             100.0%; Score 21; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35pp; English
                                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                                                                            ВP
                                                                                                                                                                                                                                                                    209
                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                              G
                                                                                        adenocarcinoma; leukaemia; Alzheimer's disease; micro
                                                                                                                                                                                                                                                                                                                                                               266 T; 0 other;
                                                                                                                                                                                                                                                                                                                            3.2;
                                                                                                                                       probe
                                                                                                                                                                                                                                                                                                                                        DB 24;
                                                                                                                                       SEQ
                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                       Length 1353;
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                                                                                                                                                                                                                                                                                                                  Indels
                                                                                          disease; microarray
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                                                                                                                                                                                                                                                                                                                                                                                                sequence is human
                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                 Gaps
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CC polynicleotide probes comprising a sequence selected from one of the 1490 CC sequences mentioned in the specification. The combination is useful as an CC array element in a microarray for monitoring the expression of a number of target polynicleotides. The microarray is particularly useful in the CC diagnosis and treatment of cancer and immunopathology and neuropathology. CC The microarray is useful in diagnostics and carcinogenicity studies, the convery and development, toxicological and carcinogenicity studies, CC forensics and pharmacogenomics. The microarray is also useful for CC monitoring progression of diseases and for developing sophisticated CC profiles for the effects of currently available therapeutic drugs. The CC combination is also useful for purifying a subpopulation of mRNAs, cDNAs and genomic fragments and in research and diagnostic applications. The CC combination is also useful for purifying a subpopulation of genes coding CC array can detect changes in expression in a large number of genes coding CC various diseases including cancer e.g. adenocarcinoma and leukaemia, concertion constitues of seases including cancer e.g. adenocarcinoma and leukaemia, concertion of probe of the invention of the present sequence represents a polynucleotide considered of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Combination of polynucleotide probes, useful as array elements microarray for monitoring the expression of a number of target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JAN-1998;
                                              at seqdata.uspto.gov/sequence.html?DocID=06500938B1.
                                                                       Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a combination which, comprises a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Au-Young J,
                                                                                                                      probe of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INCYTE GENOMICS INC
  2072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 1181; 65pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seilhamer
BP;
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316 A; 705
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C; 660 G; 391 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      comprises a number of elected from one of the 1490 combination is useful as an
  other;
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뭐 S Query Match Best Local S Matches 21 601 21; ب Similarity GCTCATCATCCCTTTCTCGCT 100.0%; ilarity 100.0%; Conservative 0 0; Score 21; Pred. No. : 621 21 Mismatches 3.4; DB 25; 0 Length 2072; Indels 0 Gaps 0

04-MAR-2003 ABZ42624 standard; DNA; 3274 BP ABZ42624; (first entry)

ABZ41254
ABZ44254
ABZ44254
AC ABZ4
XX
AC ABZ4
AC ABZ4
XX
AC ABZ4
AC ABZ4
AC ABZ4
XX
AC ABZ4
AC ABZ4 g protein-coupled receptor; GPCR; antigenic peptide; gene therapy; g protein-coupled receptor modulator; antibody; immune-related disease; growth-related disease; cell regeneration-related disease; AIDS; cancer; immunological-related cell proliferative disease; autoimmune disease; alterosis; infection; osteoarthritis; allergy; osteoperosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; graft versus host disease; Parkinson's disease; multiple sclerosis; pain; psoriasis; anxiety; depression; schizophrenia; dementia; mental retardation; epilepsy; asthma; tuberculosis; obesi hypertension; hypotension; renal disorder; rheumatoid art Human alpha 2b-adrenoceptor nucleotide SEQ ID NO:41. ф tuberculosis; obesity; nau rder; rheumatoid arthritis; memory loss; trauma;

Homo

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RESULT 10
ABL32075/c
ID ABL320
XX ABL320
XX ABL320
XX DT 26-MAR
XX DE Human
XX Human;
KW Human;
KW neurog
KW antiar
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                                                                                                                                                                                                                                                                                                                                                         Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes antigenic peptides (1) comprising:

(2) (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino code and (2) an isolated antibody having high specificity and high affinity compared therapy. The antigenic peptides for GPCRs or a candidate polypeptide in a sample; compared therapy. The antigenic peptides for GPCRs are useful in detecting compressions and antibodies. The peptides and antibodies are also useful for detecting the GPCRs and antibodies are useful for detecting the CC gresence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and designing drugs for creating immune-related diseases, growth-related designing drugs for creating immune-related diseases, growth-related designing drugs for cregeneration-related diseases, growth-related cell proliferative compared to a lerge of corresponding cal-related cell proliferative compared to a lerge of corresponding cal-related cell proliferative confidences, bacterial, fungal, protozoan or viral infections, corresponding cal-related cell proliferative corresponding protozoan or viral infections, corresponding cal-related cell proliferative corresponding cal-related cell proliferative corresponding protozoan or viral infections, corresponding cal-related cell proliferative call proliferative call proliferation, carried call proliferative call proliferative call proliferative call pro
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                      Matches
Human; immune system disease; cytosine methylation; antiasthrantiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
                                                                                                                                                                                           ABL32075;
                                                                                                                                                                                                                               ABL32075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 1; 523pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Burmer GC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-DEC-2000; 2000US-257144P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-DEC-2001; 2001WO-US50107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (LIFE-) LIFESPAN BIOSCIENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-AUG-2002
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                                                                                                                                                                                                                                                                                                                             189
                                                                                                             immune
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)B; ABP81780.
                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                             standard;
                                                                                                                                                                                                                                                                                                                                           GCTCATCATCCCTTTCTCGCT 21
                                                                                                                                                                                                                                                                                                                   GCTCATCATCCCTTTCTCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3274 BP;
                                                                                                                                                                                                                                                                                                                                                                                              Conservative.
                                                                                                           system
                                                                                                                                                (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             587 A; 979 C; 967 G; 741 T;
                                                                                                                                                                                                                         DNA; 6904
                                                                                                         associated
                                                                                                                                              entry)
                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brown JP;
                                                                                                                                                                                                                         ВP
                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                              Score 21;
Pred. No.
                                                                                                     gene
                                                                                                                                                                                                                                                                                                                   209
                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                     SEQ
                                                                                                   ij
                                                                                                                                                                                                                                                                                                                                                                                                          3.6;
                                                                                                                                                                                                                                                                                                                                                                                                                        DB 25;
                                                                                                 NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                   48.
                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               other;
                                                                                                                                                                                                                                                                                                                                                                                                                      Length 3274;
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                                                    antiasthmatic;
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RESULT 11
AAD28365/c
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                                                                                                                                                                                                                                                                                                                                                                      Query Match
               02-JUL-2001; 2001WO-EP07540.
                                                               WO200202809-A2
                                                                                       Homo
                                                                                                                            behavioural disorder; neurological;
                                                                                                                                           Human; cytostatic; antidepressant; adrenergic_alpha-1C-receptor; cyto;
                                                                                                                                                                     Human chemically treated genomic DNA #6.
                                                                                                                  Tourette's syndrome;
                                                                                                                                                                                                   22-APR-2002
                                                                                                                                                                                                                         AAD28365;
                                                                                                                                                                                                                                            AAD28365 standard;
                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, macular degeneration, arteriosclerosis, anaemia, cancer, sacute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6904 BP; 1326 A; 314 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid comprising fractor diagnosis and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JUN-2000; 2000DE-1032529
01-SEP-2000; 2000DE-1043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-JUL-2001; 2001WO-EP07537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acute myeloid leukaemia; Alzheimer's disease; ALDS; epilepsy;
neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (EPIG-) EPIGENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200200928-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                    sapiens.
                                                                                                         abuse;
                                                                                                                                                                                                                                                                                                1716 GCTCATCATCCCTTTCTCGCT
                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                             GCTCATCATCCCTTTCTCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 48; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Piepenbrock C,
                                                                                                                                       alpha-1C-receptor;
                                                                                                        migraine; ds.
                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                (first
                                                                                                                                                                                                                                           DNA; 6904
                                                                                                                                                                                                entry)
                                                                                                                smoking;
                                                                                                                                                                                                                                                                                                                                                      100.0%;
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                                                                                                                                                                                                                                                                                                                                                                   100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fragment of chemically modified ment of diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Berlin
                                                                                                                                                                                                                                                                                                                                           0,
                                                                                                        sant; neuroleptic; nootropic; antiaddic
cytosine methylation; therapy; alcohol:
gical; psychiatric; cancer; schizophren:
human immunodeficiency virus dementia;
                                                                                                                                                                                                                                           ВР
                                                                                                                                                                                                                                                                                                                                                  Score 21; DB;
Pred. No. 3.9;
                                                                                                                                                                                                                                                                                                 1696
                                                                                                                                                                                                                                                                                                                     21
                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                     2030 G;
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                                                                                                                                                                                                                                                                                                                                                             DB 24;
                                                                                                                                                                                                                                                                                                                                                                                3233 T; 1 other;
                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                            nootropic; antiaddictive
                                                                                                                                                                                                                                                                                                                                                            Length 6904;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene, usi
                                                                                                                                                                                                                                                                                                                                     0
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30-JUN-2000; 2000DE-1032529

01-SEP-2000; 2000DE-1043826.

for

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AAI9917
ID AAI99
XX AAI99217
AAI99917
AC AAI99
XX 18-FE
XX Human
XX Human
XX Human
XX Centr
KW Centr
KW Centr
KW GenBa
XX GenBa
XX GenBa
XX GenBa
XX 17-AE
PR 11-AE
PR 11-AE
PR 11-AE
PR 11-AE
PR 11-AE
PR 11-AE
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to nucleic acids comprising a segment of chemically pretreated DNA of adrenergic alpha-1C-receptor gene. The invention also relates to oligonucleotides or peptide nucleic acid (PNA) oligomers useful for detecting cytosine methylations. The pretreated DNA is useful for the diagnosis or therapy of behavioural disorders, neurological disorders and cancer, in particular major depressive disorder, Tourette's syndrome, schizophrenia, psychiatric and neurological disorders, smoking, drug abuse, alcoholism, personallty traits, compulsive gambling, human immunodeficiency virus dementia, migraine, behaviours in schizophrenic and schizophrenia. The nucleic acid is useful for detecting the methylation state of all CpG dinucleotides and/or single nucleotide polymorphisms (SNPs). The present sequence is human chemically treated genomic DNA.
                                                                                                                                                                                                                                                                                                Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor; polymorphic site; allelic variant; cardiovascular disease; central nervous system disease; adentylyl cyclase; MAP kinase activity; phosphorylation; inositol phosphate; alpha-2AAR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel nucleic acid useful for diagnosis and therapy of behavioral disorder, neurological disorder and cancer, comprises a sequence of segment of chemically pretreated DNA of adrenergic alpha-1C-receptor
                17-APR-2000; 2000US-0551744.
10-AUG-2000; 2000US-0636259.
19-OCT-2000; 2000US-06920,77.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01ek
                                                                             17-APR-2001;
                                                                                                                                           WO200179561-A2
                                                                                                                                                                                                                                                                                    GenBank Accession AF281308; chromosome
                                                                                                                                                                                                                                                                                                                                                                             Human alpha-2AAR encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                               18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAI99917 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6904 BP; 1326 A; 314 C; 2030 G; 3233 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 44-48; 190pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
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                                                                                                                                                                                                                                                     sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTCATCATCCCTTTCTCGCT 1696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTCATCATCCCTTTCTCGCT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                             2001WO-US12575
                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                     /*tag= a
/product= "alpha-2AAR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA; 1350 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ζ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 6904;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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disease, central nervous system disease and combinations of these. In addition, the technique may be used to predict an individual's response to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239, rauwolscine, idazoxan, tolazoline, phentolamine and combinations of these) by detecting the polymorphic shand correlating the site to a predetermined response (where the response is correlated to adenylyl cyclase, MAP kinase activity, phosphorylation or inositol phosphate levels). The present sequence is that of the human alpha-2AAR gene
                                                                                                                                                                                                                                                                                                             The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene (I)-(III) by detecting a polymorphic site, comprising; (a) obtaining a sample having a polymorphic site, comprising; (a) obtaining a sample having a polymorphic site comprising an alpha-2B, alpha2A or alpha2C or fragment or complement of; and (b) detecting a polymorphic site comprising nucleotide positions 901-909 of (I), a site comprising cytosine or guanine at position 753 of (IIV) or a site comprising (A) (ggggggggcg) or (B) (gggggggtgg) at positions 961-972 of (III). The method may be used for genotyping an alpha2B, alpha2A or alpha2C are and further used to determine whether an individual is at increased risk of developing a disease associated with alpha2B, alpha2A or alpha2, comprising detecting a polymorphic site which correlate to disease selected from cardiovascular disease and combinations of these In
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful determining whether an individual is at increased risk of developi disease associated with the corresponding receptor comprises detec a polymorphic site -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (LIGG/)
(SMAL/)
  Sequence 1350 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 7; Page 151; 163pp; English
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                                                   Accession AF281308).
199 A; 490 C; 441 G;
  220 T; 0 other;
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RESULT 13
AA159918
JD AA159918
AC AA19
XX AA19
XX Huma
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Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                  polymorphic site; allelic variant; cardiovascular disease; central nervous system disease; adenylyl cyclase; MAP kinase activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human alpha-2AAR variant encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAI99918 standard;
                                                                                                                                                                                                                                                                                                                       Homo
                                                                                                                                                                                                                                                                                                                                                                                                            phosphorylation;
                                                                                                                                                                                                                                                                                                                   sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCTCGTCATCCCTTTCTCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTCATCATCCCTTTCTCGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
/*tag= a
/product= "alpha-2AAR"
replace(753,C)
/*tag= b
                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                 inositol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA; 1350
                                                                                                                                                                                                                                                                                                                                                                                                        phosphate; alpha-2AAR; chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 272
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allele

밁 S

92.4%;

Score 19.4; Pred. No. 18

18;

DB 23;

Length

<u>,,</u>

WO200179561-A2

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RESULT 14
ABQ47500/c
ID ABQ47500 standard; DNA; 1733
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (C) (b) detecting a polymorphic site comprising nucleotide positions 901-909 (C) of (I), a site comprising cytosine or guanine at position 753 of (IIV) (C) or a site comprising (A) (99992999000) or (B) (99992092003) at positions 961-972 of (III). The method may be used for genotyping an alpha2A, alpha2A or alpha2C receptor gene and further used to determine (C) associated with alpha2B, alpha2A or alpha2 or alpha2
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                       Matches
Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular;
                                                                       Oligonucleotide
                                                                                                                12-JUL-2002
                                                                                                                                                          ABQ47500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for determining whether an individual is at increased risk of developing a disease associated with the corresponding receptor comprises detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to receptor gene (I)-(III) b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 152; 163pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (a) obtaining a sample having a polynucleotide encoding an alpha2A or alpha2C or fragment or complement of; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-APR-2000; 2000US-0551744.
10-AUG-2000; 2000US-0636259.
19-OCT-2000; 2000US-0692077.
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(SMAL/)
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                                                                                                                                                                                                                                                                                                252 GCTCGTCATCCCTTTCTCGCT
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DB; AAM52123.
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SMALL K M.
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                                                                                                                (first
                                                                       for
                                                              detecting cytosine methylation
                                                                                                            entry)
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95.2%;
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by detecting a polymorphic site,
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                                                                                                                                                                                                                                                                                                                                                                                                  Score 19.4;
Pred. No. 1
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methylation of a particular cytosine in a motif 5'-CpG-3', present in a cytosine (c) genomic sample of DNA. The sample is treated chemically to convert CC cytosine (c) but not methylated C, to uracil, then part of the genomic CC The amplicon is hybridised to two classes, each with at least one CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers CC and the degree of hybridisation to both classes is determined from the CC lasses of oligomers, the degree of methylation is calculated. The method CC is used: (i) for diagnosis and/or prognosis of side effects of the central nervous, cardiovascular, gastrointestinal and respiratory CC of the central nervous, cardiovascular, gastrointestinal and respiratory CC polymorphisms (SNP's), and (ii) for differentiation or single nucleotide types and for investigating cell differentiation. The method allows the CC methylation status of many C residues to be determined simultaneously. CC method for determining the degree of cytosine methylation described in XX c.
          Sequence 1733 BP; 271 A; 211 C; 625 G; 626 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                          Determining the degree of cytosine methylation in genomic DNA, for diagnosis and prognosis, comprises selective hybridization amplicons from chemically treated DNA -
                                                                                                                                                                                                                                                                                                                                                                                             Claim 12; 56pp + Sequence Listing; 56pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-SEP-2000; 2000DE-1043826.
05-SEP-2000; 2000DE-1044543.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gastrointestinal; respiratory system; single nucleotide polymorphism;
SNP; cell differentiation; ds.
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밁 Ş Matches Query Match Best Local 1222 1 GCTCATCATCCCTTTCTCGCT 21 20; Similarity GCTCGTCATCCCTTTCTCGCT 1202 92.4%; ilarity 95.2%; Conservative 0 Score 19.4; Pred. No. 18; Mismatches B 24; ۲. Length Indels 0 Gaps

0

RESULT 15 ABQ47501

ABQ47501 standard; DNA;

ABQ47501;

12-JUL-2002 (first entry)

Oligonucleotide for detecting cytosine methylation SEQ ID NO

Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism SNP; cell differentiation; ds.

WO200218632-A2.

Homo sapiens.

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This invention describes a novel method for determining the degree of CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a CC genomic sample of DNA. The sample is treated chemically to convert CC cytosine (C) but not methylated C, to uracil, then part of the genomic CC DNA that contains the target C is amplified to form a labeled amplicon. CC The amplicon is hybridised to two classes, each with at least one CC member, of oligonuclectides and/or peptide-nucleic acid (PNA) oligomers CC and the degree of hybridisation to both classes is determined from the CC label on the amplicon. From the ratio of labels hybridised to the two CC classes of oligomers, the degree of methylation is calculated. The method is used: (1) for diagnosis and/or prognosis of side effects of the central nervous, cardiovascular, gastrointestinal and respiratory contents etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation. The method allows the methylation status of many C residues to be determined simultaneously. ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method disclosure of the invention.
                                                                                                                                                 Sequence 1733 BP; 626 A; 625 C; 211 G; 271 T; 0 other;
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05-SEP-2000; 2000DE-1044543.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 12; 56pp + Sequence Listing; 56pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA -
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188 20; Conservative 0; Mismatche
512 GCTCGTCATCCCTTTCTCGCT 532
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Search completed: February 12, 2004, 04:01:23 Job time : 111.378 secs

17/5 A GO 8/97 (450/6)

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4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

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US-09-489-847-53
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Sequence 1181, Ap
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parent No. 6500938
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                                                 APPLICANT:
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                                                                             quence 1953, Application US/09313294A
tent No. 6476212
                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION UNMBER: 37,071
REFERENCE/DOCKET NUMBER: PA.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                             TOPOLOGY: line
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
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APPLICATION NUMBER:
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APPLICANT: Jeffrey J. Seilhamer
APPLICANT: Jeffrey J. Seilhamer
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STATE: CALIFORNIA
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SYSTEM: PC-DOS/MS-DOS
                                   Laura
                                                                                                                                                                                                                                                                                                                                                                                                                           (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INCYTE PHARMACEUTICALS, INC.
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                                                                                                                                                                                                                                                                                                                                         single
POLYNUCLECTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
                                              Raghunath V.
                                                                                                                                                                                                                              92.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     PA-0002 US
                                                                                                                                                                                                                            Score 19.4;
Pred. No. 2
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                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                       Length 3604;
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RESULT 5
US-09-252-991A-16352/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA;
; TYPE: DNA;
; CARNISM: Zea mays;
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6476212 700551803H1
US-09-313-294A-1953
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                                      SEQ ID NO 16352
LENGTH: 1500
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                                                                                                                                                                                                                                                                                             Sequence 16352, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Microsoft Word Version 7.0A SEQ ID NO 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 199-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL PROGRAM
SEQ ID NO 1953
LENGTH: 297
                                                                      PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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Best Local
                                                                                                                              CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                               APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: O'KEEF, DANIEL
TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE ENZYMES
FILE REFERENCE: CL-1128-A
CURRENT APPLICATION UNMER: US/09/248,335
CURRENT FILING DATE: 1999-02-10
EARLIER APPLICATION NUMBER: 08/924,759
EARLIER APPLING DATE: 1997-September-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ·09-248-335-51/c
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ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: maize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
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90.0%; Pred. No. 4
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95.0%;
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Pred. No. 6
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FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR PELICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 16239
LENGTH: 1584
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16239
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US-09-252-991A-16239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Nucleic Acids Encoding Polypeptides NUMBER OF SEQUENCES: 16 CORRESPONDENCE ADDRESS: ADDRESSEE: No. 5821100
                                                                                                                         OPERATING SYSTEM: DOS
SOFTWARE: FABESEQ for Windows Version
CURRENT APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: AGTIS, Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 46
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                               APPLICATION NUMBER: US/08/784,651
FILING DATE: 21-JAN-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                 CITY: New York STATE: NY
                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                                                                                                                                                    ZIP: 10174
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                                                                                                                                                                                                   Diskette
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Pred. No. 4
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Pred. No. 42;
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                                                                                                                                                                                                                                                                                                                                                                                                 ; LENGTH: 1860
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-489-847-53
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US-08-993-228-11
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                                                                                                                                                               Sequence 11,
Patent No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 53
LENGTH: 1860
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Best Local Similarity
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/489,847
CURRENT FILING DATE: 2000-01-24
EARLIER APPLICATION NUMBER: PCT/US99/17130
EARLIER FILING DATE: 1999-07-29
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EARLIER APPLICATION NUMBER: 60/095,455
EARLIER FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EARLIER APPLICATION NUMBER: 60/095,486
EARLIER FILING DATE: 1998-08-05
EARLIER APPLICATION NUMBER: 60/096,319
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EARLIER FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EARLIER FILING DATE: 1998-08-12 EARLIER APPLICATION NUMBER: 60/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rosen et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: 98 Human Secreted Proteins
                                                                                               APPLICANT:
APPLICANT:
                   APPLICANT:
                                                   APPLICANT:
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   TITLE OF
                                                                                                                                 APPLICANT:
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   INVENTION:
                                                                                                                                                                                                                                                                                                  GCTCATCATCCCTTTCTCGCT 21
                                                                                                                                                                                Application US/08993228
     Merberg, David
Treacy, Maurice
Spaulding, Vikki
Agostino, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/09489847
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                               McCoy, John M.
LaVallie, Edward
                                                                                 Racie, Lisa A
                                                                                                                               Jacobs,
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94.4%;
                                                                                                                                 Kenneth
                                                                                                                                                                                                                                                                                                                                                  77.1%;
85.7%;
, Michael J. SECRETED PROTEINS AND POLYNUCLEOTIDES
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Pred. No. 82
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Pred. No. 68
                                                                                                                                                                                                                                                                                                                                   Mismatches
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CORRESPONDENCE ADDRESS TITLE OF INVENTION:

ENCODING THEM

ADDRESSEE:

Inc.

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Query Match
Best Local Similarity 8:
Matches 18; Conservati
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                                                                                                                                                                                                          SOFTWALL
SEQ ID NO 9
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                                                                                                                                                                                                                                                  TITLE OF INVENTION: DETERMINATION OF GENETIC SEX IN EQUINE SPECIES TITLE OF INVENTION: DETERMINATION OF GENETIC SEX IN EQUINE SPECIES FILE REFERENCE: Wade et al CURRENT APPLICATION NUMBER: US/09/462,561B CURRENT FILING DATE: 2000-03-22 PRIOR APPLICATION NUMBER: P07802 PRIOR APPLICATION NUMBER: P07802 PRIOR APPLICATION NUMBER: P07802 PRIOR FILING DATE: 1997-07-09 PRIOR FILING DATE: 1997-07-09 PRIOR FILING DATE: 1998-07-08 PRIOR FILING DATE: 1998-07-08 PRIOR FILING DATE: 1998-07-08 PRIOR FILING DATE: 1998-07-08 PRIOR P
                                       NAME/KEY: unsure
LOCATION: (1110)
OTHER INFORMATION:
                                                                                                                                             ORGANISM: Equus caballus
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -09-462-561B-9/c
                                                                                                                                                                                                    TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Springer, Suzanne A.
REGISTRATION NUMBER: 41,323
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US/08/993,228
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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5. 6455252
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(1656)
                              unsure
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King, Brian W.
Reed, Kenneth C.
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87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           U.S.A.
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85.7%;
                                       position
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Pred. No. 87;
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APPLICANT:

Glenn, Matthew Havukkala, Ilkka J. Blokaberg, Leonard, N. Lubbers, Mark W. Dekker, James

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CURRENT APPLICATION NUMBER: US/09/511,625B
CURRENT FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: PCT/US98/17821
PRIOR FILING DATE: 1998-08-27
PRIOR APPLICATION NUMBER: 60/070,397
PRIOR APPLICATION NUMBER: 60/070,397
PRIOR FILING DATE: 1998-01-05
PRIOR FILING DATE: 1998-01-05
PRIOR FILING DATE: 1997-08-27
INCHER OF SEQ ID NOS: 70
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 414
TYPE: DNA
ORGANISM: Artificial Sequence
                                      US-09-634-238-178/c
                                                         RESULT 12
GENERAL INFORMATION:
           Sequence 178, Application US/09634238 Patent No. 6544772
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US-09-511-625B-21/c
                                                                                                                                               Matches
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APPLICANT:
APPLICANT:
                                                                                                                                                                                             OTHER INFORMATION: Description of artificial OTHER INFORMATION: synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Pierce, Jacalyn H.
TITLE OF INVENTION: ATTENDATED AND DOMINANT NEGATIVEVARIANT
TITLE OF INVENTION: CDNAS OF STAT6: STAT6b AND STAT6c
FILE REFERENCE: 14014,030011
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LOCATION: (2781)
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                                                                                  340 rcagcarrecrrecreser 322
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                                                                                                         3 TCATCATCCCTTTCTCGCT 21
                                                                                                                                            l Similarity
17; Conserv
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5. 6368828
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16; Conserv
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94.1%;
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                                                                                                                              Score 15.8; DB 4
Pred. No. 1e+02;
0; Mismatches
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Pred. No. 1.1e
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                                                                                                                                                       DB 4;
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                                                                                                                             Indels
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Christensson, Anna

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RESULT 13
US-08-784-651-1/c
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LENGTH: 1322
Query Match 75.2%;
Best Local Similarity 89.5%;
Matches 17; Conservative
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CURRENT APPLICATION NUMBER: US/09/634,238
CURRENT FILING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Polynucleotides, materials incorporating TITLE OF INVENTION: them and methods for using them.
                                                                                                                                                                                        TELEPHONE: 212-867-0123
TELEPAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tent No.
                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: AGY16, Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 46
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/784,651
FILING DATE: 21-JAN-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA:
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Berka, Randy
APPLICANT: Boominathan, Karuppan
APPLICANT: Sandal, Thomas
TITLE OF INVENTION: Nucleic Acids Encoding Polypeptides
                                                                                               TOPOLOGY: linear MOLECULE TYPE: Genomic DNA
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CORRESPONDENCE ADDRESS:
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                                                                                                                                 STRANDEDNESS:
                                                                                                                                                     LENGTH: 2168 base pairs
TYPE: nucleic acid
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STATE: NY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  405 Lexington Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IBM Compatible
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                                                                                                                                   single
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                   Score 15.8; DB 1; Length 2168; Pred. No. 1.3e+02;
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                                                                           ; OTHER INFORMATION: n = a, US-09-511-625B-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-511-625B-5/c
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Patent No. 6368828
                                                                                                                                                                                                                                                                     SOFTWARE:
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 17; Conserv
Query Match 75.2%;
Best Local Similarity 89.5%;
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/511,625B
CURRENT FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: PCT/US98/17821
PRIOR FILING DATE: 1998-08-27
PRIOR APPLICATION NUMBER: 60/070,397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Cahoon, Edgar B.
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Hitz, William D.
APPLICANT: Kinney, Anthony J.
TITLE OF INVENTION: ACYL-COA Oxidase Homologs
FILE REFERENCE: BB-1175
                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 70
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 1998-0
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1997-0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/342,647A
CURRENT FILING DATE: 1999-06-29
EARLIER APPLICATION NUMBER: 60/092,482
EARLIER FILING DATE: 1998-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Pierce, Jacalyn H.
TITLE OF INVENTION: ATTENDATED AND DOMINANT NEGATIVEVARIANT
TITLE OF INVENTION: CDUAS OF STAT6: STAT6b AND STAT6c
FILE REFERENCE: 14014.0300ul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                            OTHER INFORMATION: Description of artificial Sequence:/No. 6368828e
OTHER INFORMATION: Synthetic construct
NAME/KEY: misc feature
LOCATION: (1) (17425)
                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                   ENGTH: 17425
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Pred. No. 1.
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 Score 15.8; DB 4;
Pred. No. 1.7e+02;
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Page 6

Search completed: February 12, 2004, 06:07:47 Job time : 40.6829 secs B 8 3 TCATCATCCCTTTCTCGCT 21 ||| || || ||| ||| || || || 6,790 TCAGCATTCCTTTCTCGCT 6772

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Result
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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/cgn2_6/ptodata/1/pubpna/US09B PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US10A PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US10A PUBCOMB.seq:*
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  6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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US-10-001-073-1

US-10-305-720-1181

US-10-325-567A-41

US-10-311-455-48

US-10-001-073-24

US-10-001-073-24

US-10-001-073-25

US-10-305-720-1180

US-10-225-567A-39
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US-09-825-923-3
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US-09-825-923-1
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Sequence 1, Appli
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Sequence 3, Appli
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Sequence 11, Appli
Sequence 11, Appli
Sequence 41, Appl
Sequence 44, Appl
Sequence 25, Appl
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16.2	0	16.2	9	16.2	16.2	16.2	16.2	16.2	16.2	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4		16.4		16.4		16.8	17	17	17.4
77.1		77.1	77.1	77.1	77.1	77.1	77.1	77.1	77.1	78.1	78.1	78.1	78.1	78.1	78.1	78.1	78.1			œ	78.1	8	8	80.0		81.0	81.0	82.9
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Sequence 3, App11 Sequence 28507, A			Sequence 14649, A	14649,		134859	6869,	e 3223,	2749	Sequence 6, Appli	43	۲,	<u>ب</u>	Φ	e 42	ω ω		53	e 29,	e 15,	e 13,	e 480,	æ	æ	æ	æ	æ	Sequence 64, Appl

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## ALIGNMENTS

Sequence 13, Application US/10001073

Publication No. US20030113725A1

GENERAL INFORMATION:
APPLICANT: Liggett, Stephen
APPLICANT: Small, Kirsten
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REFERENCE: 13073-PCT
CURRENT APPLICATION NUMBER: US/10/001,073
CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13
LENGTH: 21

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; Sequence 1, Application US/09825923
; Patent No. US20010016338A1
; GENERAL INFORMATION:
; APPLICANT: Snapir, Amir
; APPLICANT: Heinonen, Paula
; APPLICANT: Alhopuro, Pia
; APPLICANT: Karvonen, Matti
; APPLICANT: Koulu, Markku
                                                                                                                               RESULT 2
US-09-825-923-1
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-001-073-13
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Best Local Similarity 100.
Matches 21; Conservative
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RESULT 4
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NAME/KEY: CDS
LOCATION: (1)..(1341)
OTHER INFORMATION: Coding sequence for variant human
OTHER INFORMATION: alpha-2B-adrenoceptor protein
3-09-825-923-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/077,870
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: FI 20010323
PRIOR FILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 10
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APPLICANT: Valkonen, Veli-Pekka
TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
TITLE OF INVENTION: protein, and uses thereof
FILE REFERENCE: Alpha-2B-AR variant
CURRENT APPLICATION NUMBER: US/09/825,923
CURRENT FILING DATE: 2001-04-05
CURRENT FILING DATE: 2001-04-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 09/422,985
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 10
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APPLICANT:
                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: (1)..(1341)
OTHER INFORMATION: Coding sequence for variant human alpha-2B-adrenoceptor protein
                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.1 EQ ID NO 1
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ORGANISM: Homo sapiens
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Salonen, Riitta
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Salonen, Jukka T
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Pred. No.
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Pred. No. 3.8;
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SEQ ID NO 3
                                                                                          Query Match
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CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2.4
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                                                                                                                                                                                                                                                                                                                                              APPLICANT: Kauhanen, Jussi
APPLICANT: Valkonen, Veli-Pekka
APPLICANT: Valkonen, Veli-Pekka
TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
TITLE OF INVENTION: protein, and uses thereof
FILE REFERENCE: Alpha-2B-AR variant
CURRENT APPLICATION NUMBER: US/99/825,923
CURRENT FILING DATE: 2001-04-05
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APPLICANT:
                                                                                                                         TYPE: DNA
ORCANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1350)
OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor
OTHER INFORMATION: protein
                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 09/422,985
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 10
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ORGANISM: Homo sapiens
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                               1 GCTCATCATCCCTTTCTCGCT
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                                                                             Similarity
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Salonen, Riitta
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Scheinin, Mika
Salonen, Jukka T
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Alhopuro, Pia
Karvonen, Matti
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                                                           Conservative
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                                                                          Score 21;
Pred. No. :
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209
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                                                            Mismatches
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RESULT 8
US-10-305-720-1181
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; ORGANISM: Homo sapiens
US-10-001-073-1
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PRIOR FILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 3.1
SEQ ID NO 3
                                                                                                  Sequence 1181, Application US/10305720 Publication No. US20040010136A1 GENERAL INFORMATION:
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Publication No. US20030113725A1
GENERAL INFORMATION:
APPLICANT: Liggett, Stephen
APPLICANT: Small, Kirsten
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Publication No. US20030003470A1
GENERAL INFORMATION:
APPLICANT: Salonen, Jukka T
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CURRENT FILING DATE: 2001-11-01
                                     APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene
FILE REFERENCE: PA-0002-1 CON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.0
CURRENT APPLICATION NUMBER: US/10/305,720 CURRENT FILING DATE: 2002-11-26
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CURRENT FILING DATE: 2002-05-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1350)
OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
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es 21; Conserv
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100.0%; Pred. No. 3.
vative 0; Mismatches
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; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank ID No. US20040010136A1 g178197
US-10-305-720-1181
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APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases As
TITLE OF INVENTION: Cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
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NUMBER OF SEQ ID NOS: 1490
SOFTWARE: PERL Program
SEQ ID NO 1181
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Publication No. US20030143606A1
GENERAL INFORMATION:
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LENGTH: 32
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Publication No.
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Best Local 9
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PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
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CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
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APPLICANT: Roush, Christine L.

TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
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ORGANISM: Homo sapiens
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TYPE: DNA
ORGANISM: Homo sapiens
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No. US20030113798A1
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ID NO 48

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; TYPE: DNA; Homo sapiens US-10-001-073-25
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US-10-001-073-25
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APPLICANT: Liggett, Kirsten
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REFERENCE: 13073-PCT
CURRENT APPLICATION NUMBER: US/10/001,073
CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 25
LENGTH: 1350
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                                        Query Match
Best Local Similarity
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CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 24
LENGTH: 1350
TYPE: DNA
TYPE: DNA
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Best Local Similarity 95.2%;
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Publication No. US20030113725A1
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APPLICANT: Small, Kirsten
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REFERENCE: 13073-PCT
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Best Local :
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NAME/KEY: unsure
LOCATION: 821
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GCTCATCATCCCTTTCTCGCT 21
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95.2%;
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Pred. No. 23
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Pred. No. 2:
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FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: Patentin version 3.1
SEQ ID NO 39
LENGTH: 3653
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       밁
                                                                                                                                 ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-39
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US-10-305-720-1180
                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 39, Appropriate Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
TITLE OR INVENTION: Composition for the Detection of Signaling Pathway Gene Expressio
FILE REFERENCE: PA-0002-1 CON
CURRENT APPLICATION NUMBER: US/10/305,720
CURRENT FILING DATE: 2002-11-26
PRIOR APPLICATION NUMBER: 09/016,434
PRIOR FILING DATE: 1998-01-30
NUMBER OF SEQ ID NOS: 1490
SOFTWARE: PERL Program
SEQ ID NO 1180
LENGTH: 3604
                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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Best Local Similarity 95.2%;
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                                                                                                                                                                                                                                                                                                                         APPLICANT: Burmer, Glenna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: LifeSpan Biosciences
APPLICANT: Brown, Joseph P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: GenBank ID No. US20040010136A1 g178195
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GCTCGTCATCCCTTTCTCGCT 1151
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Pred. No. 22;
0; Mismatches
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RESULT 15
US-10-311-455-46/c
US-10-311-455-46/c
; Sequence 46, Application US/10311455; Publication No. US20030143606A1
; GENERAL INFORMATION:

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APPLICANT: OLEK, Alexander

APPLICANT: PIEPENBROCK, Christian

APPLICANT: BERLIN, Kurt

TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ

FILE REFERENCE: 5013.1014

CURRENT APPLICATION UNMBER: US/10/311,455

CURRENT FILING DATE: 2002-12-16

PRIOR APPLICATION NUMBER: DCT/EDD1/07537

PRIOR FILING DATE: 2001-07-02

PRIOR FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: DE 10032529.7

PRIOR FILING DATE: 2000-09-01

NUMBER OF SEQ ID NO 46

LENGTH: 7353

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Chemically treated genomic DNA (Homo sapiens)

US-10-311-455-46
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Search completed: February 12, 2004, 06:15:35 Job time: 124.341 secs
                                                                                                                                                                                                Query Match 92.4%; Score 19.4; DB 13; Length 7353; Best Local Similarity 95.2%; Pred. No. 22; Matches 20; Conservative 0; Mismatches 1; Indels 0;
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Result
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AW916723 EST348027
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AUTHORS
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## ALIGNMENTS

NITION QV0-B70263-101299-072-h10 B70263 Homo sapiens cDNA, mRNA sequence.

SSION B0302172

B0302172.1 GI:20817694

EST.

Homo sapiens (human)

RCE Homo sapiens (human)

RCANISM Homo sapiens (chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

RENCE 1 (bases 1 to 297)

THORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Magai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Collveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Laboratory of Cancer Genetics

Laboratory of Cancer Genetics

Laboratory of Cancer Genetics

Laboratory of Cancer Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

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REMARK
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AUTHORS
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                                                                                                                                                           USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI TOShiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LD DNA Sequencing by: Institute for Systems Biology http://www.systemsbiology.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        262 GCTCGTCATCCCTTTCTCGCT 282
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 73 Row: o Column: 16
This clone was selected for full length sequencing because it
                                                                                                               contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton,
Madan, Stephanie Rodrigues, Amy Sanchez
                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (31-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ш
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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IMAGE:5266354,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtm12.pl?tl=QV0&t2=QV0-BT0263-
101299-072-h10&t1=1999-12-10&t4=1)
Seq primer: puc 18 forward
Seq primer: puc 18 forward
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High quality sequence stop: 205.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone
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/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
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95.2%;
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Pred. No. 3.7e+02;
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                                                                                                          Mark Ketteman, Anurac
and Michelle Whiting
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                                                                                                                                                                                                                                                                                                                                     Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                  Tacture.

1 (Dases 1 to 619)

1 (Dases 1, Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J., Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J., Kerlavage, A.R. and Adams, M.D.

Rat Genome Project: Generation of a Rat EST (REST) Catalog &
                      Similarity
                                                                                                                                                                                                                                                                                         Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                    This clone is available through the ATCC, tel#703-365-2700 for further information
                                                                                                                                                                                                                                                                                                                                                                           The Institute for Genomic Research 9712, Medical Center Drive, Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Lee,
                                                                                                                                                                                                                                                                                                                                                                                                                          Gene Index
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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AW916723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        passed the following selection criteria: matched mRNA This clone has the following problem: frame shifted. Location/Qualifiers
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                                                                      /note="Vector: pBlueScript SK(-); Site 1:
Xho1; Estimated insert size approx.1 kb"
203 c 177 g 134 t
                                                                                                                            /clone_lib="Rat gene index, normalized rat, norvegicus, Bento Soares"
                                                                                                                                                       /tissue_type="mix - brain, ov:
liver, embryo, heart, muscle,
/lab_host="SOLR"
                                                                                                                                                                                              /db_xref="taxon:10116"
/clone="RGIDT95"
                                                                                                                                                                                                                               organism="Rattus norvegicus"
|mol_type="mRNA"
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813 c 721 g 470 t
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/db_xref="taxon:9606"
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                    87.6%;
95.0%;
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    Score 18.4; D
Pred. No. 1.3e
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Pred. No. 8.
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1.3e+03;
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Unpublished
Contact: Dean RA
Clemson University Genomics Institute
                                                                                          Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe. 1 (bases 1 to 676)
Yu,Y., Zhu,H., Boyd,C.A., Gaudette,B., Gayle,A., Kingsbury,R., Phillips,K., Sasinowski,M, Wing,R.A. and Dean,R.A.
                                                                                                                                                                                        Magnaporthe grisea (anamorph: Pyricularia grisea)
Magnaporthe grisea
                                                                                                                                                                                                                                                                             AQ448022

676 bp DNA linear GSS 08-APR-1999
mgxb0016A14f CUGI Rice Blast BAC Library Magnaporthe grisea genomic
clone mgxb0016A14f, genomic survey sequence.
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1 (bases 1 to 658)
Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
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                                                                                                                                                                                                                               AQ448022.1 GI:4577159 GSS.
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Fax: 301-838-0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cdtown@tigr.org
DNA is from a doubled haploid provided by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Chris Town
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                                                                            BAC End Sequencing Framework to Sequence the Magnaporthe grisea
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/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
/note="DNA inserted into pHOS1 using BstXI linkers"
a 84 c 159 g 204 t
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/clone="BOMDM37"
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/strain="TO1000DH3"
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95.0%;
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oleracea genomic clone BOMDM37,
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Fax: 864 656 4293
Email: rdean@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
Class: BAC ends
                                                                                                                                                                                                                                           9712 Medical Center Drive,
Tel: 301-838-3523
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; eurosids II; Brassicales; Brassicaceae; Brassica. 1 to 839)

Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M. Whole genome shotgun sequencing of Brassica oleracea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brassica oleracea
Brassica oleracea
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100 Jordan Hall, Clemson Universiy, Clemson, SC 29634
                                                                                                                              Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                                             Contact: Chris
                                                                                                                                                                                                                                                                                                                                                                                                   Other_GSSs: BOGVT08TF
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  primer: TR
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/lab host="E. coli DH10B"
/clome_lib="CUGI Rice_Blast_BAC Library"
/clome_lib="CUGI Rice_Blast_BAC Library"
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                                                                1. .839
                                                                                       Location/Qualifiers
organism="Brassica oleracea"
/mol_type="genomic DNA"
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95.0%;
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Pred. No. 1.4e+(
0; Mismatches
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RESULT 8
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PUDCT72TD ZM 0.6 1.0 KB Zea mays genomic clone ZMMBTal57L24, BZ752631
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PUDCT72TB ZM 0.6 1.0 KB Z
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B2752626
B2752626.1 GI:28904975
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Similarity 95.0%;
Conservative
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Zea mays
Zea mays
Zea mays
Zea mays
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
                                                                                                                                                                                                                                                                                                                                                  Seq primer: TR
Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                                               9712 Medical Center Drive, Rockville, MD 20850, USA Tal: 301-838-5843 Fax: 301-838-0208
                                                                                            CTCATCATCCCTTTCACGCT 552
                                                                                                                                                                                                                                                                                                                                                                         Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clade; Panicoideae; Andropogoneae;
1 (bases 1 to 909)
Whitelaw C.A., Quackenbush, J., van
A., Fraser, C.M., Yuan, Y., San Migu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
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/db xref="taxon:4577"
/clone="ZMMBTa157L24"
/clone lib="ZM_0.6_1.0 KB"
/clone ="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
CoT selected genomic DNA library"
CoT selected genomic DNA library"
                                                                                                                                                                                                                                                                                      /organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
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/db xref="taxon:3712"
/clone="BOGVT08"
/clone lib="BOGV"
/clone lib="BOGV"
/note="Vector: pHOS1; Site 1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
a 106 c 200 g 259 t
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95.0%;
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The Institute of Genetics and Develo
Nanyitiao 3, Zhongguancun, Haidian,
Location/Qualifiers
                                                                                                                                                                                                                  Suo,J., Liang,X. and Xue,Y.
The construction of a cDNA library
hirsutum and its EST analysis
                                                                                                                                                                                                                                                                             Gossypium hirsutum (upland cotton)
Gossypium hirsutum
Gossypium hirsutum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.

[ Dases I to 458)
                                                                                                                                                                                    Contact: Suo J
                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                  AJ514080
AJ514080 Gossypium hirsutum ovule first day the flower opens Gossypium hirsutum cDNA clone suo86d07r3, mRNA sequence.
AJ514080
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
(labe; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 945)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick
Maize Genomics Consortium
Maize Genomics Consortium
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Email: whitelaw@tigr.org
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/mol type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBTa157L24"
/clone="ZMMBTa157L24"
/clone="YECTOF"
/note="Vector: pCR4-TOPO; Site_1: Ec
COT selected genomic DNA library"
a 183 c 174 g 293 t
                           /organism="Gossypium hirsutum mol type="mRNA" (cultivar="Zhongmian12"
/db_xref="taxon:3635"
/clone="suo86d07r3"
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ORGANISM
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Best Local
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                                                                   19;
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Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              505 bp DNA linear GS
1e24c01.g2 WGS-ZmaysF (DH5a methyl filtered) Zea mays
1e24c01 5', genomic survey sequence.
BZ374377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mccombie@cshl.org
Plate: ie24 row: c column: 01
Seq primer: -21M13UnivRev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rabinowicz,P.D., O'Shaughnessy,A.L., Ballja,V., Dedhia,N.,
Katzenburger,F., King,L., Miller,B., Muller,S., Nascimento,L.,
Zutavern,T., McCombie,W.R. and Martienssen,R.A.
Genomic shotgun sequences from Zea mays (methyl-filtered)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoldeae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PO Box 100, Cold |
Tel: 516 367 8884
Fax: 516 367 8874
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
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GCTCATCATCCCTCTCTCTCT 458
                                GCTCATCATCCCTTTCTCGCT 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     quality sequence stop: 505.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Annenberg Hazen Genome Sequencing Center Spring Harbor Laboratory ox 100, Cold Spring Harbor, NY 11724, USA
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                                                                                                                                                   /clone lib="WGS-ZmaysF (DH5a methyl filtered)"
/clone lib="WGS-ZmaysF (DH5a methyl filtered)"
/note="Organ: immature ears; Site_1: Xba I; Site_2: Xba I;
The vector was digested with XbaI and one nucleotide was added by fill in in the recessive 3' end. The genomic DNA was nebulized, end repaired, adaptor ligated and size fractionated using sephadex. The resulting fragments were between 0.8 and 3 kb and were cloned into the vector (.x/y reads in M13mp19, .b/g reads in pUC19). The same ligation was transformed into DH5a."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="first day the flower opens" /clone_lib="Gossypium hirsutum ovule first day the flower opens"
                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA"
/cultivar="B73"
                                                                                                                                                                                                                                                                                                                                   /lab_host="DH5a"
                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:4577"
/clone="ie24c01"
                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Zea mays"
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                                                                                                  DB 29;
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PSR7068 ITEC PSR Wheat Pericarp/Testa Library Triticum aestivum cDNA clone PSR7068, mRNA sequence.
BE427478
                                                                BE427478
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Anderson,O.D., Chao,S., Chin,A., Close,T.J., Crossman,C., Gustafson,J.P., Lazo,G.R., Pham,J., Rausch,C.J., Ross,K., Wilson,C. and Woo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WHE3360_A09 A18ZS Chinese Spring aluminum-stressed root tillibrary Triticum aestivum cDNA clone WHE3360_A09_A18, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequences have been trimmed to remove vector sequence quality sequence with phred score less than 20 Seq primer: SK primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 5105595773
Fax: 5105595818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Triticum.
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                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                  /note="vector: Lambda Uni-ZAP XR, excised phagemid;
Site 1: EcoRI; Site 2: XhoI; Plants were grown for four
days under hydroponTc conditions with 1ppm aluminum, root
tips were excised and snap frozen, and total RNA was
prepared at University of Missouri in the JP Gustafson lab
(Ross). Poly(A) RNA was purified, a cDNA library was made,
and the cDNA clones were in vivo excised to give
pBluescript SK(-) phagemids in the TJ Close lab (Chin) at
the University of California, Riverside. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="WHE3360_A09_A18"
/tlssue_type="Root tip at 1.0 to 1.5
/tlssue_type="RootIng"
/lab_host="E. coli SOLR"
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/db_xref="taxon:4565"
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/mol_type="mRNA"
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90.5%;
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Contact: Olin Anderson
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service,
West Area, Western Regional Research Center
Ron Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                         Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae; Triticeae; Triticum.

1 (bases 1 to 718)
Anderson,O.D., Chao,S., Chin,A., Close,T.J., Crossman,C., Gustafson,J.P., Lazo,G.R., Pham,J., Rausch,C.J., Ross,K., Wilson,C. and Woo
                                                                                                                 genomes - C
Unpublished
                                                                                                                                                      The structure and
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Triticum aestivum
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International Triticeae EST Cooperative
http://wheat.pw.usda.gov/genome.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
Contact: Bailey P
Cereals Group, John Innes Centre
Norfolk, Norwich NR4 7UH UNITED KINGDOM
Tel: 44 1603 452571 ext. 2587
Fax: 44 1603 502241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T., Cloutier,S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A., Gustafson,P., Herrmann,R.G., Holton,T., Jacquemin,J.M., Jia,J., Joudrier,P., Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P., Ogihara,Y., Pecchioni,N., Qualset,C., Schuch,W., Selvaraj,G., Shariflou,M., Sorrells,M., Warburton,M. and Wenzel,G.
International Triticeae EST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae
; Triticeae; Triticum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTCATCATCCCTTTTCCGCT 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Triticum aestivum (bread wheat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   190
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                                                                                                                                Chinese Spring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="pericarp/testa"
/dev_stage="3:1 mix 10:20 days post anthesis"
/clone lib="ITEC PSR Wheat Pericarp/Testa Library"
/note="Vector: Lambda ZAP II (Stratagene)"
122 c 160 g 162 t 16 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cultivar="Novosibirskaya 67"
/db_xref="taxon:4565"
/clone="PSR7068"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Triticum aestivum"
/mol_type="mRNA"
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90.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GI:9425321
                                                                                                                         function of the expressed portion Spring aluminum-stressed root tip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ٥,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 17.8; DB 10
Pred. No. 2.4e+03;
0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                               718 bp mRNA linear EST 29-AUG-2002
s Spring aluminum-stressed root tip cDNA
cDNA clone WHE3361_A09_B17, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 10;
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                                                                                                                     of the wheat cDNA library
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AUTHORS
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ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
VERSION
KEYWORDS
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RESULT 14
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DEFINITION
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ORIGIN
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Best Local S
Matches 19
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         397 GCTCATCATCCCTTTTCCGCT
Fax: 510 486 6798

Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003459: arm:2R [17805870,18105620]
estimated-cyto:59B2-59D2: 04/10/2001
Plate: GH 105 row: D column: 3
High quality sequence stop: 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ephydroidea; L. Ephydroidea; L
                                                                                                                                                                                                                                          Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA
                                                                                                                                                                                                                                                                                                                                                                             Unpublished
On Sep 2, 1998 this sequence version replaced
Other_ESTs: GH10539.3prime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Hexapoda, Inse
Neoptera, Endopterygota, Diptera, Brachycera,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AII13972 817 bp mRNA linear EST 23-APR-2006H10539.5prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH10539 5 similar to CG12781: FBan0012781 located on: 2R 59B4-59B4;: 04/10/2001, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                             Contact: Stapleton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AI113972.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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Fax: 5105595818
Email: oandersn@pw.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        quality sequence with phred 
Seq primer: SK primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequences have been trimmed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCTCATCATCCCTTTCTCGCT 21
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Site 1: EcoRI; Site 2: XhoI; Plants were grown for four
days under hydroponIc conditions with ippm aluminum, root
tips were excised and snap frozen, and total RNA was
prepared at University of Missouri in the JP Gustafson lab
(Ross). Poly(A) RNA was purified, a cDNA library was made,
and the cDNA clones were in vivo excised to give
pBluescript SK(-) phagemids in the TJ Close lab (Chin) at
the University of California, Riverside. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol
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/lab_host="E. coli SOLR"
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/cultivar="Chinese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GI:13757849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Triticum aestivum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84.8%;
90.5%;
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Pred. No. 2.5e+03;
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                                                                                                                                                                                                                                              94720,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Evans-Holm, M.,
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                                                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                                                                                                                                                                                                                            gi:3514775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Su, C., Tsang, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST 23-APR-2001
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RESULT 15
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VERSION
KEYWORDS
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    Query Match 84.1
Best Local Similarity 90.1
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
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ISM Hordeum vulgare subsp. vulgare

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae

; Triticeae; Hordeum.

I (bases 1 to 971)

Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T., Cloutier

,S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A., Gustafson,P.,

Herrmann,R.G., Holton,T., Jacquemin,J.M., Jia,J., Joudrier,P.,

Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P., Ogihara,Y.,

Pecchioni,N., Qualset,C., Schuch,W., Selvaraj,G., Shariflou,M.,

Sorrells,M., Warburton,M. and Wenzel,G.

International Triticeae EST Cooperative (ITEC): Production of

Expressed Sequence Tags for Species of the Triticeae

Lumpublished (2000)

Contact: Herrmann RG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       407
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HWM003.D11 ITEC HWM Barley Leaf Library Hordeum vulgare subsp.
vulgare cDNA clone HWM003.D11, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Herrmann RG
Botanisches Institut der LMU
Menzinger Str. 67, D-80638 Munchen GERMANY
Fax: 49 30 171683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: herrmann@botanik.biologie.uni-muenchen.de
International Triticeae EST Cooperative (ITEC)
http://wheat.pw.usda.gov/genome.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTCCTCCTCCCTTTCTCGCT 427
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/dev_stage="adult"
/lab_host="DH5 - alpha"
/clone_lib="GH Drosophila melanogaster head pOT2"
/clone_lib="GH Drosophila melanogaster head pOT2"
/note="Organ: head; Vector: pOT2; Site_1: EcoRI; Site_2:
/note="Organ: head; Vector: pOT2; Site_1 EcoRI; Site_2: pOT2; Site_2: pOT2; Site_1 EcoRI; Site_2: pOT2; S
                                                                                                                                                                                                                                                                 /db_xref="taxon:112509"
/clone="HWM003.D11"
/clone="HWM003.D11"
/ctssue_type="leaf"
/ctssue_type="14 day old"
/clone_lib="ITEC HWM Barley Leaf Library"
/note="Vector: pBluescriptSK(-); 850 bp average insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Hordeum vulgare
/mol_type="mRNA"
/cultivar="barke"
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/clone="GH10539"
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Pred. No. 18 the number of results predicted by chance to have a

REFERENCE AUTHORS TITLE

Liggett, S.B. and Small, K.M. Alpha-2 adrenergic receptor polymorphisms Patent: WO 0179561-A 14 25-OCT-2001;

Homo sapiens (human) Homo sapiens Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

VERSION KEYWORDS SOURCE ORGANISM

AX350502 Sequence 14 AX350502 AX350502.1

from Patent WO0179561.

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Identification in islets of Langerhans
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AAVISLPPLIYKGDQGDQPRGRPQCKLNQEAWYILASSIGSFRAPCLIWILVYLRIYL
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IAKKSNRRGPRAKGGPGQGESKQPRDHGGALASVASAREWNGHSKSTGE
KEEGETPEDTGTRALPASWAALPNSGQGQKEGVCGGSPEDEAEEEEEEEEECEPQAVP
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Eukaryota;
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Original source text: Human adult ne Draft entry and computer-readable se kindly submitted by A.C.Chang, 20-SEP-1990.
Institute of Neuroscience 155, Sect II, Li-Noon St.
Talpei, Taiwan, 11221 ROC.
Location/Qualifiers
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Homo sapiens
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Chang, A.C., Ho, T.F. and Chang, N.C.
In vitro amplification by polymerase chain reaction of a gene encoding the third subtype of alpha-2 adrenergic rec
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tissue_type="neural"
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Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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SOURCE
ORGANISM
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                                        RESULT 6
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2 (bases 1 to 1030)
2 abarovsky,E.R.
Direct Submission
Submitted (16-MAY-2001) Microbiology
Submitted (16-MAY-2001) Microbiology
                                                                                                                                               21;
              AF316895
Homo sapiens alpha
                                                                                                                                                                                                                                                                        Alpha-2 adrenergic receptor polymorphisms
Patent: WO 0179561-A 2 25-OCT-2001;
Liggett, Stephen B. (US); Small, Kersten
Location/Qualifiers
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1 (bases 1 to 1030)

Kutsenko, A.S., Gizatullin, R.Z., Al-Amin, A.N., Wang, F., Kvasha, S.M., Podowski, R.M., Matushkin, Y.G., Gyanchandani, A., Muravenko, O.V., Levitsky, V.G., Kolchanov, N.A., Protopopov, A.I., Kashuba, V.I., Kisselev, L.L., Wasserman, W., Wahlestedt, C. and Zabarovsky, E.R. NotI flanking sequences: a tool for gene discovery and verification of the human genome
                                                                                                                                                                                                                                                                                                               Liggett, S.B. and Small, K.M. Alpha-2 adrenergic receptor
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="NB1-8185"
a 329 c 308 g 182
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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3, Box 280, Stockholm 171 77,
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Small, K.M., Brown, K.M., Forbes, S.L. and Li
Direct Submission
Submitted (26-OCT-2000) Internal Medicine,
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1 (bases 1 to 1344)

Small, K.M., Brown, K.M., Forbes, S.L. and Liggett, S.B.

Polymorphic deletion of three intracellular acidic residues of the alpha 2B-adrenergic receptor decreases G protein-coupled receptor kinase-mediated phosphorylation and desensitization biological control of the series of the kinase-mediated phosphorylation and desensitization biological control of the series of the kinase-mediated phosphorylation and desensitization biological control of the series of the seri
Homo sapiens (human)
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LPNSGQGQKEGVCGASPEDEAEEEEEEEEEEEECEPQAVPVSPASACSPPLQQPQGSRVLA
TLRGQVLLGRGVGAIGGQWWRRRAQLTREKRFTFVLAVVIGVFVLCWFPFFFSYSLGA
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APQNLFLVSLAAADILVATLIIFFSLANELLGYWYFRRTWCEVYLALDVLFCTSSIVH
LCAISLDRYWAVSRALERYNSKRTFRRIKCIILTVWLIAAVISLFPLIYKGDQAFOPRG
RPQCKLNQEAWYILASSIGSFFAPCLIMILVYLRIYLIAKRSNRRGPRAKGGPGQGES
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/product="alpha 2B adrenergic receptor"
/protein_id="AAK01635.1"
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/mol_type="genomic DNA"
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Au-Young, J. and Seilhamer, J.J.
Composition for the detection of signaling pathway gene expression
Patent: US 6500938-A 1181 31-DEC-2002;
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2072)

Lomasney, J. W., Lorenz, W., Allen, L.F., King, K., Regan, J.W., Yang-Feng, T.L., Caron, M.G. and Lefkowitz, R.J.

Expansion of the alpha 2-adrenergic receptor family: cloning characterization of a human alpha 2-adrenergic receptor subty the gene for which is located on chromosome 2

Proc. Natl. Acad. Sci. U.S.A. 87 (13), 5094-5098 (1990)
                                                                                                                                                                     alpha-2-adrenergic receptor; plasma membrane protein receptor-coupled G protein.
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Human alpha-2-adrenergic receptor (alpha-2 c2) gene,
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                                         22842 bp
Homo sapiens BAC clone RP11-139J6
AC092603 AC073396
AC02603.2 GI:16303510
                                                                                                                                                                                                          1 AAAGCCCCACCATGGTCGGGT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (29-MAY-1997) INSERM Unit 317, CHU Rangueil, Toulouse 31403, France Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 9842)
Cayla,C., Schaak,S., Bouloumi
Alpha2C2-adrenergic receptor
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Homo sapiens alpha2B-adrenergic
complete cds
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Cayla, C., Schaak, S.,
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sapiens (human)
sapiens
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LPNSGQGQKEGVCGASPEDEAEEEEEEEEEEEEEEECEPQAVPVSPASACSPPLQQPQGSR
VLATLRGQVLLGRGVGAIGGQWWRRRAQLTREKRFTFVLAVVIGVFVLCWFPFFFSYS
                                                                                                                                                                                                                                                                                                                                                                                                                                  / translation="MDHQDPYSVQATAAIAAAITFIIIPTIFGNALVIIAVCTSSSLR
APQNLFLVSLAAADILVATLIIPFSLANELLGYWYFRRTWCEVVLALDVLFCTSSIVH
LCAISIDRYMAVSRALEYNSKRTPRRIKCIILTVWLIAAVISLPPLIYKGDQGFQPRG
RPQCKLNQEAWYILASSIGSFFAPCLIMILVYLRIYLIAKRSNRRGPRAKGGPGQGES
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db_xref="GI:2245628"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 product="alpha28-adrenergic receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene="alpha2C2AR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     codon start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="adrenergic receptor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene="alpha2C2AR"
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                                                                              sequence
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                                                                                                                                                                              Submitted (01-MAR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 6 On Oct 20, 2001 this sequence version replaced gi:14916188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MO 63108, USA
4 (bases 1 to 22842)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (23-OCT-2001) Genome
                                                                                                                                                                                                                                                                                                                                                                                                             5 (bases 1 to 22842) Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (20-OCT-2001) Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Waterston, R.H.
Direct Submission
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The sequence of Homo sapiens BAC clone RP11-139J6
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
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Sulston, J.E. and Waterston, R.
                                                                                                                                                                                                                                                        Direct Submission
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------ Summary Statistics
Center project name: H_NH0139J06
Drafting Center: WIBR
                                                                                             Center: Washington University Genome
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
                                                                     Contact: sapiens@watson.wustl.edu
                                                                                                                                                              ----- Genome Center
                                                                                        http://genome.wustl.edu/gsc
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                                                                                                                                                                                                                                                                                                                                          Sequencing Center, Washington 4444 Forest Park Parkway, St.
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest. This sequence was finished as follows unless otherwise noted:

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

# SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Freng Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either Research Genetics, Inc. (http://www.resgen.com) or Pieter de and coworkers at http://www.chori.org Frengen, E., one male from Jong

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The
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/db_xref="taxon:9606"
/chromosome="2"
                                 note="match to EST BF475329 (NID:gl1546156)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ocation/Qualifiers
 note="similar to Homo sapiens EST T39448 (NID:g647179)
                                                                                                       note="match to EST
                                                                                                                       2378. .12902
                                                                                                                                                                      note="match to EST AI733093 (NID:g5054206) oj40h05.x5"
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                                                                                                                                     note="match to EST AA887330
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                                                                  (NID:g11546156)"
                                                                                                    (NID:g5339305) oj40h05.y5"
                                                                                                                                   (NID:g3002438) oj40h05.s1"
                                                                                                                                                                                                                                       VERSION
KEYWORDS
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                                                                                                                                                            HTG; HTGS PHASE2.

Drosophila melanogaster (fruit fly)

Drosophila melanogaster

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AAAGCCCCACCATGGTCGGGT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 100.0%; Score 21; DB 9; I Similarity 100.0%; Pred. No. 9.9; 21; Conservative 0; Mismatches (
                                                           Rockville, MD, USA
Rockville, MD, USA
This sequence was identified as CDM:10210696 by the submitter.
This sequence was identified as CDM:10210696 by the submitter.
For more information on this record e-mail to NOTE: This is a 'working draft' sequence * This sequence will be replaced * by the finished sequence as soon as it is av the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                 81920
Drosophila melanogaster, ***
ACO19709
                                                                                                                   Direct Submission Submitted (30-DEC-1999) Celera Genomics,
                                                                                                                                                                                                                                                                                          AC019708.1
                                                                                                                                                   dams, M. and Venter, J.C.
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|14060..14247
|/note="similar to Homo sapiens EST AL549866
(NID:g12886265)"
|14060..14247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="match to EST AA836522 (NID:g2910841) od22d08.s1"
7173 c 6248 g 4624 t
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14900. .15218
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(NID:g12933576)"
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NID:g8082456)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D., Ferriera, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A., Gonzalez, M., Houck, J., Hoskins, R.A., Hoskin, D., Howland, T.J., Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattei, B., Moshrefi, A., McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunco, J., Pacleb, J., Paragas, V., Park, S., Patel, S., Pfeiffer, B., Phouanenavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F., Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M., Sequencing of Drosophila chromosome 3R, region 97A-97A
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                                                                                                                                     This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence
                                                                                                                                                                                                                                                                                                                                                              Submitted (29-JUL-1999) Drosophila Genome Center, Lawrence Laboratory, MS 64-121, Berkeley, CA 94720, USA On Feb 27, 2001 this sequence version replaced gi:6633919.
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1 (Calniker, S. E., Adams, M. D., Kronmiller, B., Tyler, D., Wan, K. H., Celniker, S. E., Adams, M. D., Kronmiller, B., Tyler, D., Wan, K. H., Celniker, S. E., Adams, M. D., Rogers, J. D., Amanatides, P. G., Brandon, R. C. Rogers, Y., An, H., Baldwin, D., Banzon, J., Besson, K. Y., Busam, D. A., Carlson, J. W., Center, A., Champe, M., Davenport, L. B., Dietz, S. M., Carlson, J. W., Center, A., Champe, M., Davenport, L. B., Dietz, S. M.,
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                                                                                                                                                                                                                                                                                                                 Sequence submitted by:
Berkeley Drosophila Genome Project
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                                                                                                                                                                                                                                                         Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
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                                                                                d relationship to other sequences, please visit our sequence
chive Web site (http://www.fruitfly.org/sequence/) or send email
bdgp@fruitfly.berkeley.edu.
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This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Celniker,S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G., Butenhoff,C., Champe,M., Chavez,C., Chew,M., Ciesiolka,L., Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L., Loskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dodson,K., Dorsett,V., Doup,L.E., Doyle,C., Dresnek,D., Farfan,D., Ferriera,S., Friee,E., Galle,R.F., Garg,N.S., George,R.A., Gonzalez,M., Houck,J., Hoskins,R.A., Hostin,D., Howland,T.J., Ibegwam,C., Jalali,M., Kruse,D., Li,P., Mattel,B., Moshrefi,A., McIntosh,T.C., Moy,M., Murphy,B., Nelson,C., Nelson,K.A., Nunoo,J., Paccleb,J., Paragas,V., Park,S., Patel,S., Pfeiffer,B., Phouanenavong,S., Pittman,G.S., Puri,V., Richards,S., Scheeler,F., Stapleton,M., Strong,R., Svirskas,R., Tector,C., Williams,S.M., Zaveri,J.S., Smith,H.O., Rubin,G.M. and Venter,J.C.
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                                                                                                                                                                                              Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS
Berkeley, CA 94720
                                                                                                                                                                                                                                                                                                                                                          Laboratory, MS 64-121, Berkeley, CA 90 On Feb 24, 2001 this sequence version
                                                                                                                                                                                                                                                                                                                                                                                            Submitted (29-JUL-1999) Drosophila Genome Center, Laboratory, MS 64-121, Berkeley, CA 94720, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, Pfeiffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E., Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zaveri, J.S., Smith, H.O., Rubin, G.M. Sequencing of Drosophila chromosome
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1 (bases 1 to 181905)
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                                                                                                                                                                                                                                                                                                                         Sequence submitted by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neoptera; Endopterygota; Diptera; Brachycera;
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Location/Qualifiers
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/mol type="genomic DNA"
/strain="y; cn bw sp"
/db xxef="texon:7227"
/db xxef="texon:7227"
/chromosome="3R"
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Compugen Ltd.
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ABQ87681 ABA90193 ABX33717	AAH46862 AAS36182 AAS36183	AAT58505 AAV84039 ABQ81032	AAS28640 AAH46866 ABX72202 AAD41400	AAV50431 AAS59566 AAL28410 AAI85859 AAQ71655	AAK53307 AAK53308 AAK61088 AAK52324 AAK52323 ABQ93524	ABX70470 AAD47687 ABA17086 ABZ19949 AAV50488	ACA56583 ABZ42624 AAS92399 ABV071991 ABA12198 AAI98095	AAQ14151 AAT59499
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# ALIGNMENTS

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RESULT 1
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XX AA19
XX AA19
XX Huma
XX Huma
XX Huma
XX Huma
XX Poly
KW Cent
XX Poly
KW Po
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10-AUG-2000; 2000US-0636259
19-OCT-2000; 2000US-0692077
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Liggett SB,
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                                                                                               (LIGG/) LIGGETT S B. (SMAL/) SMALL K M.
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     Small KM;
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disease associated with the a polymorphic site -

whether

an

, 2A, or 2C adrenergic receptor gene useful for individual is at increased risk of developing a the corresponding receptor comprises detecting

alpha-2B,

Genotyping an

WPI; 2001-611728/70

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32100/с
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splice
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02-MAY-2001; 2001US-287724P
                Shoshan
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                                                                                                                                                         07-FEB-2002.
                                                                                                                                                                                                                   Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 21
                                                                                                                                                                                      WO200210449-A2
                                                                                                                                                                                                                                                                                                Rat spliced
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                                               (COMP-) COMPUGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates
                                                                                                                                                                                                                                                  variant;
                                                                                                                                                                                                                                                                 mouse;
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                                                                                                                                                                                                                                                                                                                                                                                             standard; DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP;
              Wasserman
                                                                                                                                                                                                                                                                                                transcript detection oligonucleotide SEQ ID NO:4848
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                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                 rat; splice transcript; detection; RNA transcript;
t; transcriptome; oligonucleotide library; ss.
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by detecting a polymorphic s
                Mintz
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, or 2C adrenergic site, comprising;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , comprising;
an alpha-2B,
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Matches 21
                                                                                                                                                                                                                                                                                                                                         detecting RNA transcripts and splice variants of human or animal transcriptomes. The libraries may also be used as specialised mini libraries to detect transcripts of a sub-transcriptome under a particular biological or pathological state, and so allowing the detection of tissue- and pathology-specific genes such as those genes only expressed in specific tissue under a specific pathological condition; to detect developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from rats, humans and mice, which are used in the exemplification of the present invention.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridising selectively to a set of messenger RNAs transcribed from a given transcription unit of set of messenger RNAs transcribed from a given transcription unit of set of messenger RNAs transcribed from a given transcription unit of set of messenger RNAs transcribed from a given transcription unit of set of messenger RNAs transcribed from a given transcription unit of set of messenger RNAs transcribed from a given transcription unit of set of messenger RNAs transcribed from a given transcription unit of set of messenger RNAs transcribed from a given transcription unit of set of messenger RNAs transcribed from a given transcription unit of set of messenger RNAs transcribed from a given transcription unit of set of messenger RNAs transcribed from a given transcribed from tr
                                                                                                                                                                                                                                         Sequence 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the genome, which encodes one or more messenger RNA splice variants. The oligonucleotide libraries are useful for detecting mRNAs from a biological sample, in expression profiling studies, in qualitatively or quantitatively characterising the corresponding transcriptome, and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription a genome, useful for detecting tissue-, pathology-, and
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                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences.
                                                                                               21;
                                                                                                                                  Similarity
AAAGCCCCACCATGGTCGGGT
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                                                                                           Conservative
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RESULT 3
AAD04761/c
ID AAD0477
XX AAD0477
XX AAD047
XX AAD047
XX Human;
XX Human;
XX Human;
XW Glutam
KW norepi
KW norepi
KW corona
KW acute
XX Homo 8
XX Ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; cardiant; gene therapy; alpha2B-adrenoceptor; alpha2B-AR; glutamic acid repeat; intracellular loop; chromosome 2; catecholamine; norepinephrine; epinephrine; therapy; vascular contraction; variant; coronary artery; coronary heat disease; CHD; chronic angina pectoris; acute myocardial infarction; AMI; Prinzmetal's variant; ds.
                                                                                                                                                                   WO200129082-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-JUL-2001
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                                                                                                                                                                                                                                                              /*tag= a
/product= "Human alpha2B-adrenoceptor (alpha2B-AR)
variant protein"
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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Snapir A,
Scheinin I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clinically expressed as coronary heat disease (CHD), unstable chronic angina pectoris which is clinically expressed as Prinzmetal's variant form or acute myocardial infarction (AMI). Alpha2B-AR gene is used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New DNA molecule encoding variant specific adrenoceptor protein with deletion of specific amino acids located in the third intracellular loop of the polypeptide, for treating vascular contraction of coronal
                                                                                                                                                                                                                                                                                                                                   Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor; polymorphic site; allelic variant; cardiovascular disease; central nervous system disease; adenylyl cyclase; MAP kinase activity; phosphorylation; inositol phosphate; alpha-2BAR; chromosome 2; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1344 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human alpha-2BAR third intracellular loop variant encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first
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                                                   /*tag= a "alpha-2BAR" /product= "alpha-2BAR" /note= "sequence is deleted for a 9 nucleotides ! polymorphic site found at nucleotides ! of the wildtype alpha-2BAR protein (AA)
                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA; 1344 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21
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T, Lakka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     266 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22;
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Nyyssoenen
                                                              protein (AAI99905)
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en K;
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                                                                                          901-909
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RESULT 5
AAD44388/c
ID AAD443
XX
AC AAD443
XX
T 13-DEC
XX
DB Human
XX
KW Human;
KW hypert

13-DEC

2002

(first

entry)

AAD44388

AAD44388 standard; DNA; 1344

Human; hypertension; alpha-2B-adrenoceptor; hypertension; hypotensive; variant; gene; di Human alpha-2B-adrenoceptor variant DNA

hypotensive; variant; gene; ds

AR;

antihypertensive;

밁 S

21;

0

Mismatches

0

Indels

0

Gaps

0

AAAGCCCCACCATGGTCGGGT

666 21 Similarity

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CC (b) detecting a polymorphic site comprising uncleotide positions 901-909 CC of (I), a site comprising cytosine or guanine at position 753 of (IIV) CC or a site comprising (A) (gggggggcg) or (B) (gggggggtgg) at CC positions 961-972 of (III). The method may be used for genotyping an CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine CC whether an individual is at increased risk of developing a disease cascociated with alpha2B, alpha2A or alpha2, comprising detecting a CC polymorphic site which correlate to disease selected from cardiovascular CC disease, central nervous system disease and combinations of these. In CC addition, the technique may be used to predict an individual's response to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine, combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239, CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239, CC rauwollscine, idazoxan, tolazoline, phentolamine and combinations of these) by detecting the polymorphic site and correlating the site to a CC predetermined response (where the response is correlated to ademylyl CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate CC levels). The present sequence is that of the third intracellular loop of the human alpha-2BAR variant, the sequence is deleted for a 9 nucleotide CC (Anigagan).
Query Match
Best Local S
Matches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-APR-2000;
10-AUG-2000;
19-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to genotyping an alpha-2B, 2A, or receptor gene (I) -(III) by detecting a polymorphic site, (a) obtaining a sample having a polymucleotide encoding alpha2A or alpha2C or fragment or complement of; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 5; Page 144-145; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       determining whether an individual is at increased risk of developing a disease associated with the corresponding receptor comprises detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for determining whether an individual is at increased risk of developing
                                                                         Sequence 1344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polymorphic site
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SMALL K
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100.0%;
ilarity 100.0%;
Conservative (
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2000US-0636259.
2000US-0692077.
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                                                                           458
                                                                         C; 400
                   Score 21; DB;
Pred. No. 1.1;
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                                                                           T; 0
                                    23;
                                                                            other;
                                      Length 1344;
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Best Local S
Matches 21
                                                                     Human; cardiant; gene therapy; alpha2B-adrenoceptor; alpha2B-AR; glutamic acid repeat; intracellular loop; chromosome 2; catecholamine norepinephrine; epinephrine; therapy; vascular contraction; coronary attery; coronary heat disease; CHD; chronic angina pectoris; acute myocardial infarction; AMI; Prinzmetal's variant; ds.
                                    CDS
                                                               Homo sapiens
                                                                                                                                        Human alpha2B-adrenoceptor (alpha2B-AR) gene.
                                                                                                                                                                      04-JUL-2001
                                                                                                                                                                                                             AAD04762 standard;
                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a method for detecting a risk of hypertension by determining the pattern of alleles encoding a variant alpha-2B-adrenoceptor (AR) protein. The methods and compositions of the invention are useful for detecting risks and targeting treatment for hypertension. The kit is also useful for selecting for clinical drug trials testing the antihypertensive effect of compounds. The present sequence is human
                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                 alpha-2B-adrenoceptor variant DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 24-26; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detecting a risk of hypertension and targeting by determining the pattern of alleles encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salonen
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Synthetic.
                                                                                                                                                                                                                                                            686 AAAGCCCCACCATGGTCGGGT 666
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)B; AAE26633.
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                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                             AAAGCCCCACCATGGTCGGGT 21
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                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                (first entry)
/*tag= a
/product= "Human alpha2B-adrenoceptor (alpha2B-AR)
protein"
                              Location/Qualifiers
                                                                                                                                                                                                           DNA;
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/product= "Human alpha-2B-adrenoceptor variant
protein"
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                                                                                                                                                                                                                                                                                                               100.0%;
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                                                                                                                                                                                                            1353
                                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                            ВP
                                                                                                                                                                                                                                                                                                               Score 21;
Pred. No.
                                                                                                                                                                                                                                                                                                                                              C; 400
                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                            No.
                                                                                                                                                                                                                                                                                                                                        G; 266 T; 0 other;
                                                                                                                                                                                                                                                                                                             1.1;
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                                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               treatment
a variant
                                                                                                                                                                                                                                                                                                                   Length 1344;
                                                                                                      catecholamine;
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RESULT 7
AA199905/c
ID AA19999
XX AA19999
XX IA-FEB
XX I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is a gene encoding human alpha2B-adrenoceptor (CC (alpha2B-AR) protein. Alpha2B-AR has a glutamic acid repeat element (CC (amino acids 298-309) of 12 glutamates, in an acidic stretch of 18 amino ccids (amino acids 294-311), located in the third intracellular loop of CC checeptor polypeptide. Alpha2B-AR gene is located on chromosome 2. (CC Alpha2-AR mediate many of the physiological effects of the ccatecholamines, norepinephrine and epinephrine. An antagonist of CC alpha2B-adrenoceptor is useful for treating a mammal suffering from CC vascular contraction of coronary arteries and a disease involving CC as coronary heat disease (CHD), unstable chronic angina pectoris which is clinically expressed as prinzmetal's variant form or acute myocardial xxx (cc infarction (AMI). Alpha2B-AR gene is used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 21
                                                                                                                                                                                                     Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor; polymorphic site; allelic variant; cardiovascular disease; central nervous system disease; adenylyl cyclase; MAP kinase activity phosphorylation; inositel phosphate; alpha-2BAR;
                                                                                                                                                                                                                                                                                                                            Human alpha-2BAR third intracellular loop encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                  18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAI99905;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAI99905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1353 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 27-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New DNA molecule encoding variant specific adrenoceptor protein with deletion of specific amino acids located in the third intracellular loop of the polypeptide, for treating vascular contraction of coronary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (JUVA-) JUVANTIA PHARMA LTD OY.
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                                                                                                                                                               sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAAGCCCCACCATGGTCGGGT 666
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M, Salonen JT,
, Kauhanen J,
                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
/*tag= a
/product= "alpha-2BAR"
/note= "sequence includes
                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000WO-FI00913.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 21; 1
100.0%; Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alhopuro P, ALTUOMAINEN T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37pp;
                                                                                                                                                                                                chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Karvonen
T, Lakka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 266 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Koulu M, Pe
Nyyssoenen
                                                                                                                                                                                                                         kinase activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pesonen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ₽,
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a 9

nucleotide polymorphic

gite

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RESULT 8
AAD44389/c
ID AAD443
XX
AC AAD443
XX
AC AAD443
XX
DT 13-DEC
XX
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                                                                                                                                                                                                                                                                                                                                                          of (I), a site comprising cytosine or guanine at position 753 of (IIV) CC or a site comprising (A) (999999990) or (B) (999995993) at CC positions 961-972 of (III). The method may be used for genetyping an CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine CC whether an individual is at increased risk of developing a disease caseociated with alpha2B, alpha2A or alpha2 comprising detecting a CC polymorphic site which correlate to disease selected from cardiovascular CC disease, central nervous system disease and combinations of these. In CC disease, central nervous system disease and combinations of these. In CC addition, the technique may be used to predict an individual's response comprising the conidine, oxymetazoline, guanabenz, UK14304, BHT933 and CC combinations of these) or antagonist (e.g. pohimbine, prazosin, ARC 239, crauwolscine, idazoxan, tolazoline, phentolamine and combinations of these) or antagonist (e.g. yohimbine, prazosin, to a correlate of the site to a predetermined response (where the response is correlated to adenylyl CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate CC levels). The present sequence is that of the third intracellular loop of the human alpha-2BAR (GenBank Accession AF009500), the sequence includes a pucleotide polymorphic site at nucleotides 901-909, absent in the CC alpha-2BAR variant (AAI99906).
                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene (I) (III) by detecting a polymorphic site, comprising; (a) obtaining a sample having a polymucleotide encoding an alpha-2B, alpha2A or ralpha2C or fragment or complement of; and (b) detecting a polymorphic site comprising nucleotide positions 901-909 of (I), a site comprising cytosine or guanine at position 753 of (IIV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disease associated with the a polymorphic site -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for determining whether an individual is at increased risk of developing a disease associated with the corresponding receptor comprises detecting
                      13-DEC-2002
                                                                                               AAD44389 standard;
                                                                                                                                                                                                                                                                                                                                                    Sequence 1353 BP; 224 A; 458 C; 405 G; 266 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Page 144; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-APR-2000; 2000US-0551744.
10-AUG-2000; 2000US-0636259.
19-OCT-2000; 2000US-0692077.
                                                           AAD44389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-611728/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liggett SB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (LIGG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-APR-2001; 2001WO-US12575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200179561-A2
                                                                                                                                                                                                 989
                                                                                                                                                                                                                                                                             21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIGGETT S B.
SMALL K M.
                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                      AAAGCCCCACCATGGTCGGGT 21
                                                                                                                                                                                               AAAGCCCCACCATGGTCGGGT 666
                                                                                                                                                                                                                                                                             Conservative
                    (first
                                                                                               DNA;
                    entry)
                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                 1353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            at nucleotides 901-909 absent in the alpha-2BAR variant (AAI99906)"
                                                                                                                                                                                                                                                                         0;
                                                                                                 ВP
                                                                                                                                                                                                                                                                                           Score 21; DB 23; Length 1353; Pred. No. 1.1;
                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                           Indels
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01-OCT-1991

US5053337-A

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RESULT 9
AAQ14151/c
DY NA SAN SON SAN AC X DE X AC X DE 
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Best Local S
Matches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ14151 standard; DNA; 2064 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1353 BP; 223 A; 459 C; 405 G; 266 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a method for detecting a risk of hypertension by determining the pattern of alleles encoding a variant alpha-2B-adrenoceptor (AR) protein. The methods and compositions of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detecting a risk of hypertension and targeting treatment
by determining the pattern of alleles encoding a variant
alpha-2-adrenoceptor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
                                                                                                                                                                                                                                                                                       Homo
                                                                                                                                                                                                                                                                                                                                                              Neurotransmission;
                                                                                                                                                                                                                                                                                                                                                                                                                             Human alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ14151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   are useful for detecting risks and targeting treatment for hypertensi
The kit is also useful for selecting for clinical drug trials testing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 27-29; 35pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200266617-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human alpha-2B-adrenoceptor gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alpha-2B-adrenoceptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-FEB-2001; 2001FI-0000323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-FEB-2002; 2002WO-FI00113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (JURI-) JURILAB LTD OY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antihypertensive effect of compounds. The present sequence is human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sapiens
                                                                                                                                                                                                                                                                                       sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2002-667063/71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypertension; alpha-2B-adrenoceptor; AR; antihypertensive; ension; hypotensive; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE26634.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAAGCCCCACCATGGTCGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAAGCCCCACCATGGTCGGGT 21
                                                                                                                                                                                                                                                                                                                                                                                                                             N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                 beta
                                                                                                                                  Location/Qualifiers
288..1752
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'product= "Human alpha-2B-adrenoceptor protein"
                                                                                                                                                                                                                                                                                                                                                          adrenaline;
                                                                                                                                                                                                                                                                                                                                                                                                                             adrenergic receptor gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 21;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 666
                                                                                                                                                                                                                                                                                                                                                       epinephrine; NGC-alpha2beta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1353;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypertension.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
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Best Local S
Matches 21
                       WPI; 1997-107576/10
                                       Hartig
                                                                                 30-OCT-1989;
30-MAY-1991;
                                                         (SYNA-)
                                                                          22-OCT-1992;
                                                                                                          22-OCT-1992;
                                                                                                                          21-JAN-1997.
                                                                                                                                           US5595880-A.
                                                                                                                                                                                             Ното
                                                                                                                                                                                                            epinephrine;
                                                                                                                                                                                                           Alpha-2b adrenergic epinephrine; signal
                                                                                                                                                                                                                                     Human alpha-2b
                                                                                                                                                                                                                                                     25-MAR-2003
06-MAY-1997
                                                                                                                                                                                                                                                                                AAT59499;
                                                                                                                                                                                                                                                                                              AAT59499 standard;
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2064 BP; 319 A; 696 C;
                                                                                                                                                                                                                                                                                                                                                                                                                            Clone NGC-alpha2beta was isolated from a human spleen genomic library by screening with a fragment of the human 5-HTIA receptor gene. The gene can be used to express recombinant receptor protein which can be used to produce antibodies for inhibition of receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated DNA encoding human adrenergic receptor - for detecting nucleic acids encoding alpha, 2-beta adrenergic receptor, for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1991-310087/42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-OCT-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NEUR-) NEUROGENETIC CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-OCT-1989;
                                                                                                                                                                                                                                                                                                                                         1084
                                        PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Fig 2; 15pp; English
                AAW11804
                                                        SYNAPTIC PHARM CORP
                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                    AAAGCCCCACCATGGTCGGGT 1064
                                                                                                                                                                                                                                                                                                                                                      AAAGCCCCACCATGGTCGGGT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          drugs.
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                                                                                                                                                                                                                                                    (updated)
(first en
                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                      89US-0428856.
91US-0707604.
92US-0965040.
                                                                                                       92US-0965040
                                                                                                                                                                                                                                adrenergic receptor genomic
                                                                                                                                                                  Location/Qualifiers
288..1751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hartig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89US-0428856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89US-0428856.
                                                                                                                                                                                                                                                                                             DNA;
                                                                                                                                                                                                        receptor; adrenoceptor; adrenaline; transduction; neurotransmitter; lig
                                                                                                                                                                                                                                                    entry)
                                                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PR;
                                                                                                                                                                                                                                                                                             2064
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                                                                                                                                                                                                                                                                                             ВP
                                                                                                                                                                                                                                                                                                                                                                              Score 21; I
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                       659
                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                      <u>ن</u>
                                                                                                                                                                                                                                                                                                                                                                                                     390 T; 0
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                                                                                                                                                                                                                                 DNA clone.
                                                                                                                                                                                                                                                                                                                                                                                   12; Length
                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                    other;
                                                                                                                                                                                                        ligand;
                                                                                                                                                                                                                                                                                                                                                                                   2064;
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                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Assay for alpha-2b adrenergic receptor ligands - using

membranes

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RESULT 11
ACAS6583/G
AID ACAS65
XX ACAS65
XX ACAS65
XX DG Human;
XW Human;
XW Human;
XW Human;
XW IMMUNO
OS Homo 8
XX US6500
XX INCY-
PF 30-JAN
XX INCY-
XX ACAS65
PF 30-JAN
XX WPI; 1
XX ACAS65
XX INCY-
XX BAL-You
XX WPI; 1
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The invention relates to a combination which, comprises a number of polynucleotide probes comprising a sequence selected from one of the 1490 sequences mentioned in the specification. The combination is useful as an array element in a microarray for monitoring the expression of a number of target polynucleotides. The microarray is particularly useful in the diagnosis and treatment of cancer and immunopathology and neuropathology. The microarray is useful in diagnostics and treatment regimens, drug discovery and development, toxicological and carcinogenicity studies,
                                                                                                                                                                                                                                                                                                                              Combination of polynucleotide probes, useful as array elements microarray for monitoring the expression of a number of target
                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 1181; 65pp;
                                                                                                                                                                                                                                                                                                                           polynucleotides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Au-Young
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; probe; ss; array element; Parkinson's disease; signalling pathway population; cancer; adenocarcinoma; leukaemia; immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; micro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-DEC-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACA56583;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seilhamer JJ;
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Pred. No.
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RESULT 12
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G protein-coupled receptor; GPCR; antigenic peptide; gene therapy; growth-related disease; cell regeneration-related disease; prowth-related disease; cell regeneration-related disease; AIDS; cancer; immunological-related cell proliferative disease; autoimmune disease; Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy; alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy; osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; graft versus host disease; Parkinson's disease; multiple sclerosis; pain; psorisais; anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea; hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            forensics and pharmacogenomics. The microarray is also useful for monitoring progression of diseases and for developing sophisticated profiles for the effects of currently available therapeutic drugs. The combination is also useful for purifying a subpopulation of mRNMs, cDNAs and genomic fragments and in research and diagnostic applications. The array can detect changes in expression in a large number of genes coding for different signaling pathway populations which can be used to diagnose various diseases including cancer e.g. adenocarcinoma and leukaemia, immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease and Parkinson's disease. The present sequence represents a polynucleotide
                                                                                                                                                                              New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease
                                                                                                                                                          cancer or autoimmune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-DEC-2001; 2001WO-US50107.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (LIFE-) LIFESPAN BIOSCIENCES INC.
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DB; ABP81780.
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                                                                                                                                                                                     Alzheimer's disease
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Disclosure;

Fig 1; 523pp; English

present invention describes antigenic peptides (I) comprising:

Claim 1; SEQ ID

No 28203; 103pp; English

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RESULT 13
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Best Local (
                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss
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23-AUG-2000;
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                                                                                                                                                                                                                                   2001-639362/73
DB; ABG28212.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21;
                                                                                                                                                                                                                                                                                                                                  RT,
                                                                                                                                                                                                                                                                                                                                                                                                  HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; ilarity 100.0%; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0540217.
2000US-0649167.
                                                                                                                                                                                                                                                                                                                              Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                              Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; 967 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ВÞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 21; DB :
Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 3274;
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Matches
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Best Local :
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16-MAR-2000;
25-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                          Novel isolated nucleic acid molecule associated with cancerous state prostate cells and correlating with presence of prostate cancer, usef
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; prostate pharmacogenomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations
    Claim 1; Page 1278; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human prostate expression marker cDNA 7982.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABV07991 standard; cDNA; 447
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                                                                                                                                                                                                                                                                                                                                                                           20-FEB-2001;
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                                                                                                                                                                                                  (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences.
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; 2000US-189862P.
; 2000US-207454P.
; 2000US-211314P.
; 2000US-219007P.
; 2000US-255281P.
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                                                                                                                                                                                                                                                                                                                                                                             2001WO-US05171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                        presence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer; cytostatic; carcinogen; pharmacodyanamic marker;
marker; gene; ss.
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94.7%;
                                        of prostate
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                                        stage
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RESULT 15
ABA12198
ID ABA122
XX ABA12
XX ABA14
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Best Local S
Matches 18
                                                                                                                                                                                          07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
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(d) assessing the efficacy of a therapy for inhibiting in a patient;
(e) selecting a composition for inhibiting prostate can (f) assessing the prostate cell carcinogenic potential (g) determining whether prostate cancer has metastasize (h) assessing the aggressiveness or indolence of program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulno antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticorvulsant; antifungal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human nervous system related polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABA12198 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neurological disease;
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                                                                                                                                                                                                                                                                                                                                          18-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    378
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2000US-0216647.
2000US-0216880.
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                                                                                                               2000US-0217487.
2000US-0217496.
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                                                         2000US-0220963
                                                                                      2000US-0218290
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2000US-0190076
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibacterial; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer;
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2000US-0225759. 2000US-0226279. 2000US-0226681. 2000US-0226868. 2000US-0227182. 2000US-0227009.

2000US-0229345. 2000US-0229509. 2000US-0229513.

2000US-0229344

2000US-0228924. 2000US-0229287. 2000US-0229343. 2000US-0225447. 2000US-0225757. 2000US-0225758. 2000US-0225759. 2000US-0226279.

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The invention relates to novel genes (ABA11004-ABA21534) and proteins CC (ABB14678-ABB18001) useful for preventing, treating or ameliorating cmedical conditions e.g. by protein or gene therapy. The genes are CC isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast CC and ovarian cancer and other cancers of the adrenal gland, bone, bone cancer of immune disorders e.g. Addison's disease, allergies, autoimmune CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (c) cardiovascular disorders such as myocardial ischaemias; (c) disease; and (f) infectious diseases such as viral, bacterial, fungal cc and parasitic infectious diseases such as viral, bacterial, fungal
                                                                                                                                                                                                                                                                                                                                                                                   17-NOV-2000
01-DEC-2000
01-DEC-2000
05-DEC-2000
05-DEC-2000
06-DEC-2000
06-DEC-2000
08-DEC-2000
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17-NOV-2000;
17-NOV-2000;
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17-NOV-2000;
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17-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                       Nucleic acids encoding useful for preventing, cancers and metastases
                                                                                                                                                                                                                                                                                          WPI; 2001-541565/60.
P-PSDB; ABB15872.
                                                                                                                                                                                                              Claim 1; SEQ ID NO 1205; 1701pp +
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17-NOV-2000;
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17-NOV-2000;
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CC Note: The sequence data for this patent did not form part of the CC printed specification, but was obtained in electronic format directly CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Squence 990 BP; 193 A; 336 C; 270 G; 188 T; 3 other;

Query Match
Best Local Similarity 94.4%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Search completed: February 12, 2004, 04:01:27

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Perfect score:
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

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4: /cgn2_6/ptodata/2/ina/FCTUS_COMB.seq:*

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                     GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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US-09-773-426A-6
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US-09-662-250A-10
US-08-469-260A-28
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US-08-467-344A-28
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US-09-252-991A-4268
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Sequence 13, Appli
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### ; LIBRARY: GENBA ; CLONE: g178197 US-09-016-434-1181 RESULT 1 US-09-016-434-1181/c CLASSIFICATION: ANTORNEY/AGENT INFORMATION: NAME: Zeller, Karen J. REGISTRATION NUMBER: 37,071 REGISTRATION NUMBER: PA-01 REFERENCE/DOCKET NUMBER: PA-01 REFERENCE/DOCKET NUMBER: PA-01 REFERENCE/DOCKET NUMBER: PA-01 REFERENCE/DOCKET NUMBER: PA-01 REFERENCE/CAPTION INFORMATION: TELEPHONE: (650) 845-4166 INFORMATION FOR SEQ ID NO: 1181: SEQUENCE CHARACTERISTICS: LENGTH: 2072 base pairs TYPE: nucleic acid Patent No. COUNTRY: USA ZIP: 94304 ZIP: 94304 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/016,434 FILING DATE: HEREWITH CLASSIFICATION: PRIOR APPLICATION DATA: APPLICATION NUMBER: PRIOR APPLICATION NUMBER: ETILING DATE: HEREWITH CLASSIFICATION NUMBER: PRIOR APPLICATION NUMBER: Query Match Best Local Similarity GENERAL INFORMATION: APPLICANT: Janice Au-Young APPLICANT: Jeffrey J. Seilhamer TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING TITLE OF INVENTION: PATHMAY GENE EXPRESSION NUMBER OF SEQUENCES: 1490 CORRESPONDENCE ADDRESS: IMMEDIATE SOURCE: STREET: 3174 PORTI CITY: PALO ALTO STATE: CALIFORNIA STRANDEDNESS: TOPOLOGY: lir FILING DATE: ADDRESSEE: INCYTE PHARMACEUTICALS, INC 1181, Apr o. 6500938 3174 PORTER DRIVE Application US/09016434 linear single 100.0%; PA-0002 US Score 21; DB 4; Pred. No. 0.18; Length 2072;

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Matches

21;

Conservative

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US-09-773-426A-13/C

Sequence 13, Application US/09773426A Patent No. 6534302

GENERAL INFORMATION:

APPLICANT: Tsia, Fong-Ying APPLICANT: Rudolph-Owen, Laura A. APPLICANT: Glucksman, Maria Alexandra APPLICANT: Williamson, Mark

Williamson, Mark Teia, Fong-Ying

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TITLE OF INVENTION: 22438, 23533, 25278, and 26212 No. 6534302el
TITLE OF INVENTION: Human Sulfatases (A CIP Application)
FILE REFERENCE: 35800/208398(5800-79
CURRENT APPLICATION NUMBER: US/09/773,426A
CURRENT FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: US 09/495,823
PRIOR PRIOR DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 14
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: MacLennan, A. John
TITILE OF INVENTION: Molecular Cloning and Expression
TITILE OF INVENTION: G-Protein Coupled Receptors
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
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US-08-760-936-1
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                                                                         RESULT 5
US-09-225-024-1
                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: DNA (genomic) US-08-760-936-1
                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/760.
APPLICATION NUMBER: US/08/760.
APPLING DATE: December 6, 1996
CLASSIFICATION: 536
CLASSIFICATION: 536
ATTORNEY/AGENT IMFORMATION:
NAME: Pace, Doran R.
REGISTRATION NUMBER: 38,261
REFERENCE/DOCKET NUMBER: MAC-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
TELEPHONE: 352-372-5800
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2754 base pairs
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Best Local
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APPLICANT: MacLennan,
Sequence 1, Application US/09225024
Patent No. 6518414
GENERAL INFORMATION:
APPLICANT: MacLennan, A. John
                                                                                                                                                                                                                       Matches
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Molecular Cloning and Expression of TITLE OF INVENTION: G-Protein Coupled Receptors NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                 LENGTH: 2754 base pairs TYPE: nucleic acid STRANDEDNESS: single
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les 17; Conserv
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2421 N.W. 41st Street, Suite A-1
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Pred. No. 70;
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Pred. No. 70;
                                                                                                                                                                                                                             Mismatches
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1070 AGACCCACCAGGGTCGGGT 1052

AGCCCCACCATGGTCGGGT 21

US-09-773-426A-13

Query Match

Local

ch 75.2%; 1 Similarity 89.5%; 17; Conservative

0; Mismatches

Score 15.8; Pred. No. 6

66; DB SEQ ID NO 13 LENGTH: 1710 TYPE: DNA ORGANISM: homo sapiens

US-08-196-989B-1 RESULT 3

Sequence 1, Application US/08196989B Patent No. 5585476

GENERAL INFORMATION:

STREET: 2421 CITY: Gainesville

EL

NDDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1

COUNTRY:

SD

32606

INFORMATION FOR SEQ ID NO:

TELECOMMUNICATION INFORMATION: TELEPHONE: 904-375-8100 TELEFAX: 904-372-5800

ATTORNEY/AGENT INFORMATION:
NAME: L10yd, Jeff
REGISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: MAC

MAC-100

CLASSIFICATION:

APPLICATION NUMBER: US/08/196,989B FILING DATE: 15-FEB-1994

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APPLICANT: Williamson, Mark
APPLICANT: Tsia, Fong-Ying
APPLICANT: Tsia, Fong-Ying
APPLICANT: Rudolph-Owen, Laura A.
TITLE OF INVENTION: 22438, 23553, 25278, and 26212 No. 653
TITLE OF INVENTION: Human Sulfatases (A CIP Application)
FILE REFERENCE: 35800/208398(5800-79
CURRENT APPLICATION NUMBER: US/09/773,426A
CURRENT FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: US 09/495,823
PRIOR APPLICATION NUMBER: US 09/495,823
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
US-09-773-426A-6/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-225-024-1
                                                                       SOFTWARE: FastSEQ
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/09773426A Patent No. 6534302 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 352-372-5800
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2754 base pairs
                                                                                                                                                                                                                                                                                                                                           APPLICANT: Glucksman, Maria Alexandra
              TYPE: DNA
ORGANISM: homo sapiens
EATURE:
                                                      ENGTH: 2940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Pace, Doran R.
REGISTRATION NUMBER: 38,261
REFERENCE/DOCKET NUMBER: MAC-100C1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: US
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/760,936
FILING DATE: 6-DEC-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: MC
TITLE OF INVENTION: G-
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 2754 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 04-JAN CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1 CITY: Galnesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PILING DATE: 15-FE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139 AGCCCCACCATGGGCGGTT 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGCCCCACCATGGTCGGGT 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75.2%;
89.5%;
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Pred. No. 7
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; LOCATION: (23)...(154)
US-09-662-250A-10
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US-09-662-250A-10
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Patent No. 6
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Best Local Similarity
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CURRENT FILING DATE: 2000-09-14
NUMBER OF SEQ ID NOS: 102
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TYPE: DNA
ORGANISM: Homo &
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Brett P. Mon:
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANT:
FILE REFERENCE: RTS-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: (334)...(2043)
                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                      TITLE OF INVENTION: NON-A, NON-B. NON-C, NON-D, NON-E HEPATITIS TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
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Local Similarity 89.5%;
hes 17; Conservative
                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                              COUNTRY: USA
ZIP: 60064-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1403 AGACCCACCAGGGTCGGGT 1385
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                                                                                                                                                                                          OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/08469260A
                                                                                                                                                                                                                                   JAMES C. ERKER
SHERI L. BUIJK
ISA K. MUSHAHWAR
                                                                                                                                                                                                                                                                                                   SURESH M. DESAI THOMAS P. LEARY
                                                                                                                                                                                                                                                                                   ANTHONY SCOTT MUERHOFF
                                                                                                                                                                                                                                                                                                                                  GEORGE G. SCHLAUDER
                                                                                                                                                                                                                                                                                                                                              GEORGE J. DAWSON
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brett P. Monia
                                                                                                                                                                                                                                                                                                                                                                                I. SIMONS
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94.1%;
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                                                                                                                                                                                                                                                                                                   LEARY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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Pred. No. 87
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Pred. No. 70;
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                                                                                                                                                           D377/AP6D
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/469,260A

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
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                                                                        FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION UMBER: US
APPLICATION NUMBER: US
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0.
                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D STREET: 100 ABBOTT PARK ROAD CITY: ABBOTT PARK
                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,446
                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: POREMBSKI PRISCILLA I
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 55:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
NAME: POREMBSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 60064-3500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 AAAGCCCCACCATAGGCCGG 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 72.4%; Score 15.2; DB 4; Similarity 85.0%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1: 369 base pairs nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                           INVENTION: NON-A, NON-B. NON-C, NON-D, NON-E HEPATITIS INVENTION: REAGENTS AND METHODS FOR THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/08488446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOHN N. SIMONS
TAMI J. PILOT-MATIAS
GEORGE J. DAWSON
GEORGE G. SCHLAUDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTHONY SCOTT MUERHOFF
JAMES C. ERKER
SHERI L. BUIJK
ISA K. MUSHAHWAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SURESH M. DESAI
THOMAS P. LEARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRISCILLA E.
                                                                                        US/08/424,550
                                                                                                                                                             US/08/488,446
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HER: 5527.PC.01
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 85.0 Matches 17; Conservative
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                                                                                                                     TELEPHONE: 708-937-6365
TELEPAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 369 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/467,344A

FILING DATE: 07-Un-1995

CLASSIFICATION: CUNknown>
PRIOR APPLICATION DATA:

APPLICATION UNUBER: 08/424,550

FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:

NAME: POREMBSKI, PRISCILLA E.

REGISTRATION NUMBER: 33,207

REGISTRATION NUMBER: 33,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
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TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 5527.PC.01 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JAMES C. ERKER
SHERI L. BULJK
SHERI L. BULJK
ISA K. MUSHAHWAR
TITLE OF INVENTION: NON-A, NON-B. NON-C,
REAGENTS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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                                                    LENGTH: 369 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 60064-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 100 ABBOTT PARK ROAD CITY: ABBOTT PARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
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TAMI J. PILOT-MATIAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GEORGE J. DAWSON
GEORGE G. SCHLAUDER
SURESH M. DESAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THOMAS P. LEARY
ANTHONY SCOTT MUERHOFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA (genomic)
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85.0%;
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Pred. No. 1.1e+02;
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FOR THEIR USE
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SEQ ID NO:

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RESULT 11
US-09-149-476-36/c
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CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: PZ002P1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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ER APPLICATION NUMBER: 60/047,492
ER FILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/047,598
ER FILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/047,613
ER FILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/047,582
ER FILING DATE: 1997-05-23
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                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 1997-0
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FILING DATE: 1997-05-23
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FILING DATE: 1997-03-07
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FILING DATE: 1997-03-07
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FILING DATE: 1997-05-23
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                                                                                                                                                           APPLICATION NUMBER: 60/047,587
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Pred. No. 1.
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ER FILLING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,878
ER FILLING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,662
ER FILLING DATE: 1997-08-22
ER FILLING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,872
ER APPLICATION NUMBER: 60/056,882
ER APPLICATION NUMBER: 60/056,637
ER APPLICATION NUMBER: 60/056,637
ER FILING DATE: 1997-08-22
ER FILING DATE: 1997-08-22
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,903
ER PILLING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,903
ER PILLING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,888
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ER APPLICATION NUMBER: 60/056,888
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              3R APPLICATION NUMBER: 60/056,911
ER FILING DATE: 1997-08-22
ER FILING DATE: 1997-08-26
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,874
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,910
ER APPLICATION NUMBER: 60/056,910
ER FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,313
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,672
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,315
R FILING DATE: 1997-04-11
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,612
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,632
                                                                                                                                                       APPLICATION NUMBER: 60/
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/
FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,877
FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/
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FILING DATE: 1997-04-11
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APPLICATION NUMBER: 60/
FILING DATE: 1997-04-11
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APPLICATION NUMBER: 60/043,580
FILING DATE: 1997-04-11
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APPLICATION NUMBER: 60/047,601
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DATE: 1997-08-22

60/056,631

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APPLICATION NUMBER: 60/056,892
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APPLICATION NUMBER: 60/047,585
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ICATION NUMBER: 60/043,576
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85.0%;
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4268
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                                                  Sequence 4200, Application US/09252991A Patent No. 6551795
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SEQ ID NO 4484
                                  GENERAL INFORMATION:
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Best Local Similarity
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Best Local
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SEQ ID NO 4268
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APPLICANT: Marc J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
 APPLICANT: Marc J. TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-252-991A-4484
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PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1998-0
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                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Pseudomonas aeruginosa
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VENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
VENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                         ID NOS:
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Rubenfield et
NUCLEIC ACID
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Pred. No. 1.2e
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Sequence 1, Application US/09050861B

Patent No. 655314

GENERAL INFORMATION:
APPLICANT: Bayan, Donald

ITILE OF INVENTION: TOSO AS A TARGET FOR DRUG SCREENING
FILE REFERENCE: RIGL-002CON

CURRENT APPLICATION NUMBER: US/09/050,861B

CURRENT FILING DATE: 1998-03-30

PRIOR APPLICATION NUMBER: US/09/651,150B

PRIOR FILING DATE: 2000-08-30

PRIOR FILING DATE: 2000-08-30

PRIOR FILING DATE: 1998-03-30

INUMBER OF SEQ ID NOS: 35

SOPTWARE: PATENTIN PATENTIN OF SEQ ID NOS: 35

SOPTWARE: PATENTIN PATENTIN VETSION 3.1

LENGTH: 1911

TYPE: DNA
ORGANISM: Homo sapiens
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CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 4200
SEQ ID NO 4200
LENGTH: 1611
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4200
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Search completed: February 12, 2004, 06:07:49 Job time: 30.6829 secs
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US-09-050-861B-1/c
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Match
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/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
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/cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
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_6/ptodata/1/pubpna/US05_PUBCOMs.seq:*
_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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US-10-010-073-1

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US-09-914-353-19559

US-09-918-995-29585

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-10-314-881-	-680-	US-10-426-776-16		US-10-212-872-1074	US-09-764-860-1074	US-10-369-493-38181	US-10-369-493-38026	US-10-369-493-35369	-10-369-493-3857	-10-027-632-	US-10-027-632-25794	-10-198	-10-369-493-	US-10-289-980-1		US-10-071-338-1	US-10-214-519-1		US-10-288-985-6	-10-071-338-	-10-214-519-	- 1	US-10-027-632-139092	US-10-027-632-139091	US-10-027-632-139092	US-10-027-632-139091	US-10-017-161-739	-790-3	US-10-094-886-137
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### ALIGNMENTS

RESULT 1 US-10-001-073-14

Sequence 14, Application US/10001073

Publication No. US2003013725A1

GENERAL INFORMATION:

APPLICANT: Liggett, Stephen

APPLICANT: Small, Kirsten

ITTLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms

FILE REFERENCE: 13073-PCT

CURRENT PILLING DATE: 2001-11-01

NUMBER OF SEQ ID NOS: 53

SOPTWARE: Patentin Ver. 2.0

SEQ ID NO 14

LENGTH: 21

TYPE: DNA

ORGANISM: Homo sapiens

US-10-001-073-14

Query Match
Best Local Similarity 100.0%; Score 21; DB 15; Length 21;

Best Local Similarity 100.0%; Pred. No. 1.9;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Sequence 4848, Application US/09908975

Publication No. US20030165843A1

APPLICANT: MASSERMAN, Avi
APPLICANT: MASSERMAN, Avi
APPLICANT: MINTZ, Liat
APPLICANT: MINTZ, Liat
APPLICANT: FAIGLER, Simchon

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US-09-825-923-1/c
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; ORGANISM: Rattus norvegicus
US-09-908-975-4848
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Matches
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Best Local Similarity
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CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 60/287,724
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/221,607
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 32337
                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 1
                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Kauhanen, Jussi
APPLICANT: Valkonen, Veli-Pekka
APPLICANT: Valkonen, Veli-Pekka
TITLE OF INVENTION: A DUA molecule encoding a variant alpha-2B-adrenoceptor
TITLE OF INVENTION: protein, and uses thereof
FILE REFERENCE: Alpha-2B-AR variant
CURRENT FILINGIATION NUMBER: US/09/825,923
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 09/422,985
PRIOR FILING DATE: 2000-05-25
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 10
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APPLICANT: Heinonen, Pa
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                                                                                                                                                            NAME/KEY: CDS.
LOCATION: (1). (1341)
OTHER INFORMATION: Coding sequence for variant human
OTHER INFORMATION: alpha-2B-adrenoceptor protein
                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
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                      1 AMAGCCCCACCATGGTCGGGT 21
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Salonen, Jukka T
Tuomainen, Tomi-Pekka
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Alhopuro, Pia
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CURRENT APPLICATION NUMBER: US/10/001,073
CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 1344
TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT: Salonen, Jukka T
APPLICANT: Salonen, Jukka T
TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
FILE REFERENCE: 0933-0183P
CURRENT APPLICATION NUMBER: US/10/077,870
CURRENT FILING DATE: 2002-05-21
CURRENT FILING DATE: 2002-05-21
                                                                                                                                                                                                                                        US-09-825-923-3/c
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Publication No. US20030113725A1
GENERAL INFORMATION:
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                                                                                                                        GENERAL INFORMATION:
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PRIOR FILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 3.1
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Best Local Similarity
                                                                                                                                                        Sequence 3, Application US/09825923 Patent No. US20010016338A1
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APPLICANT: Small, Kirsten
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REFERENCE: 13073-PCT
FILE REFERENCE: 13073-PCT
TITLE TERROR TO THE TO 
APPLICANT: Snapir, Amir
APPLICANT: Heinonen, Paula
APPLICANT: Alhopuro, Pia
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LOCATION: (1)..(1341)
OTHER INFORMATION: Coding sequence for variant human alpha-2B-adrenoceptor protein
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ORGANISM: Homo sapiens
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Similarity 100.0%;
21; Conservative 0
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Pred. No. 1.4;
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APPLICANT: APPLICANT:

Pesonen, Ullamari

Karvonen, Koulu, Markku

Matti

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RESULT 8
US-10-001-073-1/c
; Sequence 1, Application US/10001073
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                                                                                                                                                                                                                                                 US-10-077-870-3
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Publication No. US20030003470A1

GENERAL INFORMATION:
APPLICANT: Salonen, Jukka T

TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof FILE REFERENCE: 0933-0183P

CURRENT APPLICATION NUMBER: US/10/077,870

CURRENT PILING DATE: 2002-05-21

PRIOR FILING DATE: 2002-05-21

PRIOR APPLICATION NUMBER: FI 20010323

PRIOR FILING DATE: 2001-02-20

NUMBER OF SEQ ID NOS: 10

SOFTWARE: Patentin Ver. 3.1
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SEQ ID NO 3
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APPLICANT: Valkonen, Veli-Pekka
APPLICANT: Valkonen, Veli-Pekka
TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
TITLE OF INVENTION: protein, and uses thereof
FILE REFERENCE: Alpha-2B-AR variant
CURRENT APPLICATION NUMBER: US/09/825,923
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 09/422,985
PRIOR APPLICATION NUMBER: 09/422,985
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
PRIOR PILING DATE: 2000-05-25
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NAME/KEY: CDS
LOCATION: (1)..(1350)
OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor
OTHER INFORMATION: protein
                                                                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: (1)..(1350)
OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor protein
                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Salonen, Riitta
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Salonen, Jukka
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Pred. No. 1
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: GenBank ID No. US20040010136A1 g178197
US-10-305-720-1181
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TYPE: DNA
CORGANISM: Homo sapiens
US-10-001-073-1
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SOFTWARE: PERL Program
SEQ ID NO 1181
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Tocal Similarity
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TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression FILE REFERENCE: PA-0002-1 CON
CURRENT APPLICATION NUMBER: US/10/305,720
CURRENT FILING DATE: 2002-11-26
PRIOR APPLICATION NUMBER: 09/016,434
PRIOR APPLICATION NUMBER: 09/016,434
PRIOR PILING DATE: 1998-01-30
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
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APPLICANT: Small, Kirsten
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REFERENCE: 13073-PCT
CURRENT APPLICATION NUMBER: US/10/001,073
CURRENT APPLICATE 2001-11-01
RUMBER OF SEQ ID NOS: 53
                                                                                                    APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glenna C.
APPLICANT: ROUSH, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
                                                                                                                          APPLICANT: LifeSpan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glenna C.
APPLICANT: Roush, Christine L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 2072
TYPE: DNA
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Pred. No. 1.3;
0; Mismatches
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Pred. No.
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NUMBER OF SEQ ID NOS:

PatentIn version 3.1

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                                                US-09-918-995-29585/c

Sequence 29585, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
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                                                                                                                                 RESULT 12
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Best Local Similarity
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 19559
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                                                                                                                                                                                                                                                                             Query Match
Best Local 9
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TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS,
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PRE-
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REFERENCE: MRI-006B
FILE REFERENCE: MRI-006B
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TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/257,672
PRIOR FILING DATE: 2000-12-21
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APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID
TITLE OF INVENTION: FROM VARIOUS CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                      LOCATION: 4327, 4328, 4329, 4330, 4331, 4332, 4333, 4334, LOCATION: 4337, 4338, 4339, 4340, 4341, 4342, 4343, 4344, LOCATION: 4347, 4348, 4349, 4350

OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RENT FILING DATE: 2001-03-21
OR APPLICATION NUMBER: US 60/191,031
OR FILING DATE: 2000-03-21
OR APPLICATION NUMBER: US 60/207,124
OR APPLICATION NUMBER: US 60/207,124
OR FILING DATE: 2000-05-25
OR APPLICATION NUMBER: US 60/211,940
OR FILING DATE: 2000-6-15
OR APPLICATION NUMBER: US 60/216,820
OR FILING DATE: 2000-07-07
OR APPLICATION NUMBER: US 60/220,661
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                                                                                                                                                                                                                                                                                   Similarity
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Pred. No.
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Pred. No. 1.3e+02;
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     SEQUENCES
LIBRARIES
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                       OBTAINED
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4345,
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; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/99/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 29585
; LENGTH: 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GRGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(481)
OTHER INFORMATION: n = A,T,C
US-09-918-995-29585
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US-10-027-632-131352/c
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                                                                                                                                                      ; ORGANISM: Human US-10-027-632-131352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                             SOFTWARE: FastSEQ
SEQ ID NO 131352
LENGTH: 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                            Matches
                                                                                            Query Match
Best Local
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CURRENT FILING DATE: 2002-04-30
CURRENT FILING UNMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                           PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/198,676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
                                                                                                                                                                                             TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 60/156,358
  551
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l Similarity 94.4%;
17; Conservative
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                                                                            l Similarity
17; Conserv
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  AGCCCCACCATGCTCGGG
                                     AGCCCCACCATGGTCGGG 20
                                                                            Conservative
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                                                                                                94.4%;
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Pred. No. 2.3e+02;
  534
                                                                              0,
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Pred. No. 2.3e+02;
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                                                                                                                     Length 565;
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RESULT 14
US-10-027-632-131352/c
; Sequence 131352, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.

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; LENGTH: 565
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-131352
Search completed: February 12, 2004, 06:15:44
Job time: 128.341 secs
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                                                                                                                                                                                                                                                                                                                                        ; SEQ ID NO 38
; LENGTH: 2262
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-220-891-38
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US-10-220-891-38/c
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PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/199,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR PILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR PILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/166,358
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 199-09-28
PRIOR FILING DATE: 199-09-28
PRIOR FILING DATE: 199-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/220,891
CURRENT FILING DATE: 2003-03-07
PRIOR APPLICATION NUMBER: JP 2000/140387
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: JP 2000/159195
PRIOR APPLICATION NUMBER: JP 2000/159195
PRIOR FILING DATE: 2000-03-07
NUMBER OF SEQ ID NOS: 1108
SOFTWARE: Patentin version 3.2
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Best Local Similarity 94.4
Matches 17; Conservative
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 131352
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Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: NAKAGAWARA, AKIRA
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES HAVING CHARACTERITICS OF ENHANCED
TITLE OF INVENTION: EXPRESSION IN HUMAN NEUROBLASTOMA WITH FAVORABLE PROGNOSIS
TITLE OF INVENTION: BASED ON COMPARISON BETWEEN HUMAN NEUROBLASTOMA WITH FAVORABLE
TITLE OF INVENTION: PROGNOSIS AND HUMAN NEUROBLASTOMA WITH UNFAVORABLE PROGNOSIS
FILE REFERENCE: 7388-73435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                                         78.1%; Score 16.4; DB 13; Length 2262; Local Similarity 94.4%; Pred. No. 2.1e+02; nes 17; Conservative 0; Mismatches 1; Indels 0;
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                                                                                                           3 AGCCCCACCATGGTCGGG 20
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1487 AGCCCCACCATGCTCGGG 1470
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94.4%; Pred. No. 2.3e+02;
tive 0; Mismatches 1
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                               Score
  21
18.4
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21
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(without alignments)
449.373 Million cell updates/sec
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 BQ880026
AW391095
AI582395
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BQ880026 AGENCOURT
AW391095 MR3-ST020
AI582395 tr97b09.x
AU166948 AU166948
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						14	13	13	13	13	13	10	10	10	13	12	29	9	9	10	13	29	28	14	φ	14	9	13	13	12	12	12	28	12	28	φ	9	13	9	9
AA448314	BI713098	AA447622	AA448451	BE517145	AA448022	CB069817	BY200267	BY337375	BY214037	BY195012	BY149362	BF811542	BF946030	BG242458	BU587459	BQ061158	BZ551182	AL533975	AL549851	BF307809	BU603088	CNS031RL	BH794448	CB529586	AW161813	CA912228	AI494022	BX316223	BY401935	BQ053165	BM469354	BP111519	AZ571445	BI687242	BH794919	72	54	8	AL566688	32
zw96h03.s	BI713098 ie02b10.y	:w97b03.	AA448451 zw96h03.r	WHE0624	:w97b03.r	CB069817 is29e01.y	BY200267 BY200267	BY337375 BY337375	BY214037 BY214037	BY195012 BY195012	BY149362 BY149362	BF811542 CM2-CI017	BF946030 CM0-NN115	BG242458 602354253	BU587459 AGENCOURT	BQ061158 AGENCOURT	BZ551182 pacs1-60_	AL533975 AL533975	AL549851 AL549851	BF307809 601890896	BU603088 AGENCOURT	AL223914 Tetraodon	BH794448 ME_MBa000	CB529586 UI-H-FT2-	AW161813 au70g04.x	CA912228 PCSC21166	AI494022 qz97h04.x	BX316223 BX316223	BY401935 BY401935	BO053165 AGENCOURT	BM469354 AGENCOURT	BP111519 BP111519	AZ571445 287PvG04	BI687242 603314820	BH794919 ME MBa000	AI869725 wl98h12.x	AI216547 qm36h04.x	2389	566688 AL566688	19320 tf27e1

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# ALIGNMENTS

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RESULT 1
BQ880026/c
LOCUS
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Clone IMAGE:6179035 5', mRNA sequence.
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Clone IMAGE:6179035 5', mRNA sequence.
BQ880026
REFERION
REFORMENS
SOURCE
Homo sapiens (human)
SOURCE
AUTHORS
TITLE
TOURNAL
COMMENT
COMMENT
Contact: Robert Strausberg, Ph.D.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13559 row: i column: 20
High quality sequence stop: 430.

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FEATURES
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AW391095
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AUTHORS
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      261 bp mRNA linear MR3-5T0203-131299-111-f11 ST0203 Homo sapiens cDNA, AW391095
                                                                                                                                                                                                                                                                    Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR3&t2=MR3-ST0203-
131299-111-f11&t3=1999-12-13&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua prof. Antonio Prudente 109, 4 andar, 01509-010,
                                                                                                                                                                                    High quality sequence start: 10 High quality sequence stop: 63. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                              Tel: +55-11-2704922
Fax: +55-11-2707001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The FAPESP/LICR Human Cancer Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                primer: puc 18 forward
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ilarity 100.0%;
Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 kb for average insert length 1.7 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life Technologies."

1 334 c 345 g 183 t
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/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
NotI; Site 2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACGCGTCCG-3' and
5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCT[15]-3'. Size selected >
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/mol_type="mRNA"
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/dev_stage="adult, 36 yr"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'db_xref="taxon:9606"
'clone="IMAGE:6179035"
                                                         /db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="ST0203"
                                                                                                                    /organism="Homo sapiens"
/mol_type="mRNA"
/note="Organ: stomach; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 1044
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376

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 209
                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1875 Std Error: 0.00
Seq primer: -40UP from Gibco
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                                                          19;
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EST.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
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(larity 95.0%;
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                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2227001"
                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                          tissue_type="adenocarcinoma"
lab_host="DH10B"
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                                                                                                                                                                                                             _lib="NCI_CGAP_Pan1"
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                                                                          Score 17.8; DB 9;
Pred. No. 6.9e+02;
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cDNA clone IMAGE:2227001
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nes 19; Conserv
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Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Sequencing by: Washington University Genome of the Clone distribution: WCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 724)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 376)
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AU166948
AU166948.1 GI:1240
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similar to gb:X52255_rna1
                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                          (CGAP/BTGAP), Tumor Gene Index Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
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                                                                                                                                                      cDNA Library Preparation: M. Bento Soares, Ph.D.,
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Procurement: David N. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
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/clone_Tib="Rice_callus (2001)"
81 c 81 g 106 t
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/db_xref="taxon:39947"
/clone="C60162"
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/mol_type="mRNA"
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Pred. No. 7.2e+02;
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Homo sapiens cDNA clone IMAGE:2097452 3'
CYSTATIN C PRECURSOR (HUMAN);, mRNA
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High quality sequence stop:
                                                                                                                                                                                                                       http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODF019DDD6NP1&cluster=8536.r. Contact
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODF019DD06NP1.
                                                                                                                                                                                                                                                                                                                                                                                          Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
                                                                                                                                                                                                                                                                                                                                                                                                                                            Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 16, 2001 this sequence version replaced gi:12919302.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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EST.
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AL566688 Homo sapiens FETAL BRAIN Homo CSODF019YH12 3-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                   Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 8536.r
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria;
1 (bases 1 to 921)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/tissue_type="FETAL BRAIN"
/dev_stage="fetal"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/clone="Organ: brain; Vector: pCMVSPORT_6; lst strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
                                                                                                                                /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/tissue_type="glioblastoma (pooled)"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                clone="CSODF019YH12"
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90.5%;
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8e+02;
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BQ923897/c
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Matches 19
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5', mRNA sequence.
EQ923897
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cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM14009 row: g column: 22
High quality sequence stop: 413.
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NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
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AI216547
AI216547.1 GI:3785588
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                                             qm36h04.x1 NCI_CGAP_Lu5 mRNA sequence.
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184 c 269 g 176 t 61 others
                                                                                                                                                                                                                                                                                                      /clone lib="NIH_MGC_71"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_;
Site_2: SalI, Cloned unidirectionally. Primer: '
Average insert size 2.1 kb. "
Average 228 g 233 t
                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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(tissue_type="leiomyosarcoma"
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90.5%;
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ie_lib="NIH_MGC_71"
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Primates;
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Pred. No. 8.3e+02;
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Pred. No. 8.
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                                                             bp mRNA linear EST 02-DEC-1998
sapiens cDNA clone IMAGE:1883959 3',
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primer: Oligo
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Insert Length: 589 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 177.
Location/Qualifiers
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 212)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AI869725 487 bp mRNA linear EST 07-MAR-2000 w198h12.x1 NCI CGAP Brn25 Homo sapiens cDNA clone IMAGE:2432999 3' similar to gb:L11285 DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE (HUMAN);, mRNA sequence.
Unpublished
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Email: David N. Louis,
                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 487)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
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//lone lib="NCI CGAP Lu5"
//clone lib="NCI Lu5"
//cl
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/db_xref="taxon:9606"
/clone="IMAGE:1883959"
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94.7%;
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Pred. No. 1e+03;
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                             M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 212;
                             Myrna R. Rosenfeld M.D.,
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SOURCE
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BH794919
                                                                                                                                                                                                                                                                                                                                                            REFERENCE
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                                                                                                                                                                                                                                                                            New Genomic Resources for Cassava (Manihot esculenta): Development of a Deep-Coverage BAC Library and Preliminary STC Analysis
                                                                                                                                                                                                                                                                                            1 (bases 1 to 740)
Tomkins, J.P., Fregene, M., Main, D., Goicoechea, J.L., Blackmon, B., Atkins, M., Tohme, J. and Wing, R.A.
New Genomic Resources for Cassava (Manihot esculenta): Developme
                                                                                                                                                                                                                                                                                                                                                                      Manihot esculenta
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Malpighiales; Buphorbiaceae; Manihot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BH794919 740 bp DNA linear GSS 02-APR-2002 ME_MBA0003L01r Manihot esculenta Manihot esculenta genomic clone ME_MBA0003L01r, genomic survey sequence.

BH794919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AMAGECECEACCATGGTEGG 19
                                                             Email: jtmkns@clemson.edu
Total High Quality bases = 176
Total High Quality bases = 176
Seq primer: TAATACGACTCACTATAGGG
Class: BAC ends
                                                                                                                                       Tel: 864 656 6419
Fax: 864 656 4293
                                                                                                                                                                          Clemson University
100 Jordan Hall, Clemson University, Clemson,
                                                                                                                                                                                                                 Contact: Tomkins J
Clemson University Genomics Institute
                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BH794919.1 GI:19893527
GSS.
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1703 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Manihot esculenta (cassava)
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h quality sequence stop: 364.
Location/Qualifiers
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quality sequence start: 38 quality sequence stop: 514. Location/Qualifiers
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/ti8sue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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94.7%;
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Pred. No. 1.1e+03;
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ORIGIN
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                         BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                          cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11902 row: g column: 05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1485 bp
603314820F1 NCI_CGAP_Mam6 Mus mu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1485)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BI687242.1 GI:15649870
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    /db_xref="tax.on:10090"
/db_xref="tax.on:10090"
/clone="IMAGE:534908"
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/tissue_type="infiltrating ductal carcinoma"
/tissue_type="infiltrating ductal carcinoma"
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/clone_lib="NCI_CGAP_Mam6"
/clone_lib="NCI_CGAP_Mam6"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
/inte="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
/site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"
07 a 342 c 327 g 306 t 3 others
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1 216 c 158 g 191 t 1 othe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone lib="Manihot esculenta"
/note="Vector: pCUGIBAC-1; Site_1: HindIII; Site_2: NotI;
For more details on library preparation and sequence
analysis see
                                                                                                                                                                                                                                                                                            organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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To order clones from this library see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Manihot esculenta"
/mol_type="genomic DNA"
/strain="MECW72"
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/clone="ME_MBa0003L01r"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tissue_type="Leaf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'lab_host="E. coli"
                                                                                                                                                                                                                                                                                                                                                                .1485
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Pred. No. 1.2e+03;
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Query Match

82.9%;

Score 17.4;

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Length 1485;

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287FvG04 Pv MBN #30 Plasmodium vivax genomic 3', genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Dame JB
Dept. of Pathobiology, College of Veterinary Medicine
University of Florida
2015 SW 23rd Avenue, Bldg 1017, Gainesville, FL 32611, USA
Tel: 352 392 4700
Fax: 352 392 9704
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Carlton, J.M.-R. and Dame, J.B.
The Plasmodium vivax and P. berghei gene sequence tag projects
Parasitol. Today (Regul. Ed.) 16 (10), 409 (2000)
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                 696 AAAGCCCCACCATGGTC 680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: damej@mail.vetmed.uri
Seq primer: M13(-20) forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAAGCCCCACCATGGGCGG 1422
                                                                                                       Similarity
                                  AAAGCCCCACCATGGTC 17
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                                                                                                                                                                              181
                                                                                                                                                                       /cloue_ILD=_rv ream +Dv rottor DNA, phagemid /note=Twector: pBluescript SK(+) vector DNA, phagemid /note=Twector: pBluescript SK(+) visite 2: EcoR V; excised from lambda ZAP; Site 1: EcoR V; vivax Infected blood using the following methods: first, infected blood using the following methods: first, infected blood was activated by the addition of 0.5 ml of ADP (40mg/ml) was activated by the addition of 0.5 ml of ADP (40mg/ml) was activated by the addition of 0.5 ml of ADP (40mg/ml) activated by passage through a column of pre-wet filter, followed by passage through a column of pre-wet filter, followed by passage through a 50% Percoll density and finally centrifuged through a 50% Percoll density and finally centrified DNA was digested with mung bean nuclease in the presence of 44% formamide at 500c as described (vernick, K.D., Imberski, R.B., and McCutchan, T.F. 1988. (vernick, K.D., Imberski, R.B., and McCutchan, T.F. 1988. Nucleic Acids Research 16:6883-6885). Digested DNA was blunt-ended using T4 DNA Polymerase and size fractionated blunt-ended using T5 DNA Polymerase and size fractionated blunt-ended using T4 DNA Polymerase and size fractionated corer a Sepharose CL-2B column. Fractions in the size range south of the Sco RV site of pBluescript SK(+), and E. coli XL-10 Gold transformed with the ligation mixture."
                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              damej@mail.vetmed.ufl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Plasmodium vivax"
/mol_type="genomic DNA"
/strain="Salvador I (Collins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="asexual blood forms"
/lab_host="Saimiri boliviensis"
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Ishiwata, H., Katsuma, S., Kizaki, K., Patel, O.V., Nakano, H., Takahashi, T., Imai, K., Hirasawa, A., Shiojima, S., Ikawa, H., St., Tsujimoto, G., Izaike, Y., Todoroki, J. and Hashizume, K., Y., Tsujimoto of gene expression profiles in early bovine Characterization of gene expression profiles in early bovine pregnancy using a custom cDNA microarray Mol. Reprod. Dev. 65 (1), 9-18 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Gozoh Tsujimoto
Department of Molecular, Cell Pharmacology
National Research Institute for Child Health and Development
3-35-11 Taishido, Setagaya, Tokyo 154-8567, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: gtsujimoto@nch.go.jp
This work was performed to collaborate with Developmental Biology
Department, National Institute of Agrobiological Sciences. Address:
2 Ikenodai, Tsukuba, Ibaraki, 305-8602 Japan. Phone & Fax:
81-29-838-8633 e-mail: kazuha@affrc.go.jp
This work was funded by Organized Research Combination System (ORCS This work was funded by Organized Research Sports, Science and ) project of Ministry of Education, Culture, Sports, Science and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bovidae; Bovinae;
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AGENCOURT_6480665 NIH_MGC_85 Homo
5', mRNA BEQUENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 960)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished
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/dev_stage="adult"
/clone_lib="ORCS bovine utero-placenta cDNA"
/s 2 203 g 183 t 2 others
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/db_xref="taxon:9913"
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a CDNA Bos taurus CDNA clone
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RESULT 15
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                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Daniel McVicar, DBS/NCI

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

plate: LLCM2121 row: g column: 23

High quality sequence stop: 825.

Location/Qualifiers
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AGENCOURT_6821899 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5934766
5', mRNA sequence.
BQ053165
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
Clone distribution: MGC clone distribution information
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1017)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 545.
Location/Qualifiers
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Plate: LLAM12265 row: e column: 19
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/tissue_type="lymphoma, cell line"
/lab_host="DH108 (phage-resistant)"
/clone_lib="NIH_MGC_85"
/note="Organ: lymph; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.867 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
a 221 c 248 g 241 t
/clone="IMAGE:5934766"
/tissue_type="natural killer cells, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_106"
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/db_xref="taxon:9606"
                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
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/note="Organ: blood; Vector: pOTB7; Site\_1: XhoI; Site\_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

BASE COUNT ORIGIN 279

Query Match Best Local Matches Similarity Conservative 81.0%; Score 17; DB 12; Length 1017; 100.0%; Pred. No. 2e+03; <u>,</u> Mismatches ٥. Indels <u>.</u> Gaps 0

밁 ঠ 1004 AAAGCCCCACCATGGTC 988 1 AAAGCCCCACCATGGTC 17

Search completed: February 12, 2004, 06:05:52 Job time : 1142.79 secs

Mis Pogo Blonk (Uspto)

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Database :
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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta,
Neoptera, Endopterygota, Diptera, Brachycera, Muscc
Ephydroidea, Drosophilidae, Drosophila.
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45260 bp DNA linear INV 24-SEP-2002
Drosophila pseudoobscura FOSMID DPSF1-548A9 (Children's Hospital
Oakland Research Institute Drosophila pseudoobscura FOSMID Library)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartcoideae; Oryzeae; Oryza.

El (bases 1 to 15455)

Euell,C.R., Yuan,Q., Ouyang,S., Liu,J., Gansberger,K., Jones,K.M., Overton II,L.L., Tsittin,T., Kim,M.M., Bera,J.J., Jin,S.S., Fadrosh,D.W., Tallon,L.J., Koo,H., Zismann,V., Hsiao,J., Blunt,S., Vanaken,S.S., Riedmuller,S.B., Peterson,J.J., Quackenbush,J., White,O., Salzberg,S.L. and Fraser,C.M.

Oryza sativa chromosome 3 BAC OSJNBa0059E14 genomic sequence
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Submitted (24-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA Sequencing is completed to a minimum standard of double strand sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 3 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality does not meet this standard, it will be indicated in the annotation.
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Submitted (15-APR-2003) The Institute for Genomic Research,
Medical Center Dr. Rockville, MD 20850, USA
4 (bases 1 to 154555)
                                                                                                                                                                                                                                                   Direct Submission
Submitted (01-NOV-2002) The Institute for Genomic Medical Center Dr., Rockville, MD 20850, USA 3 (bases 1 to 154555)
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Medical Center Dr, Rockville, MD 20850, USA, ri
On Apr 15, 2003 this sequence version replaced
Address all correspondence to:rice@tigr.org
                         Submitted (25-APR-2003) The Institute for Genomic Research, Medical Center Dr, Rockville, MD 20850, USA, rbuell@tigr.org On Apr 15, 2003 this sequence version replaced gi:24462343.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ω
••
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 45260;
                                                                                                                                                                                                                                                                                                    Research,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLN 25-APR-2003
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clone OSJNBa0059E14 is from Oryza sativa chromosome orientation of the sequence is from SP6 to T7 end of

end of the

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bource
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                                                                                 repeat_region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This BAC overlaps with rice BAC OSJNBb0015I02 (AC135563). Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genes were identified by a combination of several methods: Gene prediction programs including Fgenesh (http://www.softberry.com/), genscan and Genscan+ (Chris Burge, http://CCR-081.mit.edu/GENSCAN.html), GeneMarkHMM (Mark Borodovsky,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://ftp.genome.washington.edu/RM/RepeatMasker.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://genemark.biology.gatech.edu/GeneMark/), and GeneSplicer (Mihaela Pertea and Steven Salzberg, contact mpertea@tigr.org),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="OSJNBa0059E14.1"

/note="EST AU165836, AU182644 from this gene"

complement (join(<2338...2570, 2665...>3123))

/gene="OSJNBa0059E14.1"

complement (join(2499...2570, 2665...3123))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="j
                               /rpt_family="(CGG)n"
9301. .11079
                                                                                                                                                                            ffagrcldddhrtladygvrhdsvvflslrlatdayqtemhvrlmqpetatakqemh
Qqqqqlhvhvaaddeekaikrkpvsrralrkilsrlqvdawtsqhdakfldlllrht
GGGGGarnvgeltgedwssiraelnaatgsgfpveelqrrlgefrrefeaasriknhp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4169. .5246
/gene="OSJNBa0059E14.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MAAIANLELSTHTHTHTQRVCSIDRPSPRAHDGERSSQPRRGGG
GDRGVCGCRGGGGGRRGRGGGVVRRRGERAGAVRAVPAGRRGAAGRSVLRRREGAARD
GGHGGGAARAVQVPGAVRAVVRRAPRPRAAPPGALQARTRHPRRRHRLQQDILSGSG
                                                                                                                   KCRETKARSCLRKLLRNFRLRFKL"
                                                                                                                                                                                                                                                                                            /codon_start=1
/product="putative ubiquitin"
/protein_id="AAP21418.1"
/db_xref="GI:30103005"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GDDDAATWREFVAIGA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="unknown protein"
/protein_id="AAP21417.1"
/db_xref="GI:30103004"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (2338.
                                                                                                                                                   RFSYDPRRRVVVAKQADWKNYILENPEAAAYEGRSPRHLGRLRAIFSGDGGGGGGGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                      /note="similar to ubiquitin GB:BAC06474 GI:22004048 (Ciona savignyi)"
(join(<4169. .4410,4495. .4975,5067. .>5246)
(gene="0SJNBa0059E14.2"
(gene="0SJNBa0059E14.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'gene="OSJNBa0059E14.1"
'codon BEATT-"
/gene="OSJNBa0059E14.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone="OSJNBa0059E14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cultivar="Nipponbare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Oryza sativa
                                                                                                                                                                                                                                                                      translation="MRIMVRTLRGDRVALDVDGATTTVAQVKGMVMARERIAVAMQRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         map="near C393A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 154555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     _xref="taxon:39947"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    family="(CCGCG)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            family="AT_rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aponica cultivar-group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (japonica cultivar-group) "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA
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repeat_region
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                                                                                                                                                                                                                                                                                                                                                                                                           17243. .17429,17725. .17991,18085. .18430,18519. .18656, 18739. .18864,18950. .19162,19322. .19577,19773. .19975, 20219. .2059, 20652. .21236)
/gene="OSJNHBA0059E14.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mote="highly similar to cellulose synthase catalytic subunit GB:AAC3936 GI:2827143 (Arabidopsis thaliana); EST AU064228,AU176398, GB096725,AA751514 from this gene" join(15663...16059,16193...16379,16712...16962,17065...171243...17429,17725...17991,18085...18430,18519...18656, 18739...184864,18950...19162,13922...19577,19773...19975, 20219...20569,20652...>21236)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_
13913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NLVAVRPDI VRGGADGPPVTVPGMPGGREITI PVSELPDFLVQDDHLSMSWDRI KASQ
LAGFGVVNNTFAALEAPYCDETSRVDARFAX YFVGEVSQPSRAAAAVRRGGDGDVDCL
RWLSTKPSQSVVYVCFGSWAHFSVTQTTRELALGLEASNQPFLMVIRSDSGDGGGENE
PEGWERRMEGRGMVVRGWAPQLAVLAHPSVGAFVTHCGWNSVLEAAAAGVPALTWPLV
FEQFINERLVTEVAAFGARVWEDGGGKRGVRAREAETVPAGVIARAVAGFMAGGGGRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9422. .955;
/rpt_family="(CCG)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MLHEQHAPPPQPEPEVSLQLSAPATAADDVAAGDDEEVTVVTTY RDIHELTPPSFTTTTPPTRLOSAAYSMOTASSHRSVSSEEQFWMSRETAMVAAGT TWOTGPNDGNNGGDQLTSIGEDELESTNPLAIVPDSHPIATPARSRASQLEVLVPPAAGT STRAPVBARQVEKEEVETKVSAWQTAEVAKINNFFKREEVVINGWETEQVEKASAWLK KIERKLDEQRAKALERTQNDIAKARRKAEEKRASAEAKRGLKLAKVLELANFMKAVGR
                                                                                                                                                                                             /translation="MDGAKSGKQCHVCQICGDGVGTAADGELFTACDVCGFPVCRPCY
EYERKDGSQACPQCKTKYKRHKGSPPILGDESDDVDADDASDVNYPTSGNQDHKHKIA
ERMLTWRWNSGRNDDIVHSKYDSGEIGHPKYDSGEIPRIYIPSLTHSQISGEIPGASP
                                                                                                  GTS1APSEGRGVGDIDASTDYNMEDALLNDETRQPLSRKVPISSSRINPYRMVIVLRL
IVLCIFLHYRITNPVRNAYPLWLLSVICEIWFALSWILDQFPKWSPINRETYLDRLAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="maaatadghggrrrlrvfflpffarghlipmtdlaclmaaastd
aveveatmavtpanaaaiaatvagnaavrvvcypfpdvglargveclgaaaahdtwrv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (12645. .14126)
/gene="OSJNBa0059E14.4"
                                                                  RYDREGEPSQLAPVDIFVSTVDPMKEPPLVTANTVLSILAVDYPVDKVSCYVSDDGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ERAAAMATALAESARVAVGENGSSWRDIRRLIQDLTDATASQP"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VPTKRSFF
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/protein_id="AAP21420.1"
/db_xref="GI:30103007"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="contains Pfam profile PF03763 (remorin, C terminal
region); EST BE041106,D41920,AU097433 from this gene"
REYEEFKVRVNALVAKAQKVPEEGWIMQDGTPWPGNNTRDHPGMIQVFLGHSGGLDTE
                                                                                                                                                          DHMMSPVGNIGRRGHPFPYVNHSPNPSREFSGSLGNVAWKERVDGWKMKDKGAIPMAN
                                                                                                                                                                                                                                                                                        product="putative cellulose synthase catalytic subunit"
/protein id="AAP21426.1"
/db_xref="GI:30103013"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="OSJNBa0059E14.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YRAVDLSRPAHESLLRHHRPDAIVADVPFWWATGVAAELGVPRLTFNPVGVFPQLAMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAP21423.1"
/db_xref="GI:30103010"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           codon_start=1
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lucosyltransferase GB:AAB36653 GI:1685005 (Nicotian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   join(9403. .10065,10558. .10749)
/gene="OSJNBa0059E14.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene="OSJNBa0059E14.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           product="putative immediate-early salicylate-induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                family="GC_rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 family="(CGG)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .14126)
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SOURCE
ORGANISM
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26680 TGATCGCCAAACAAGCAAC 26698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HIG; אויס אחסטב.
Oryza satīva (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa (japonica cultivar-group)
OSJNBA0070D14, *** SEQUENCING IN DECCENSIONAL CONTRACTOR OF CONTRACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Swain, S.C., Sureshbabu, K., Singh, A., Pal, S., Gaikwad, K., Ghazi, I.A., Dixit, A., Yadav, M., Srivastava, S., Bhargava, A., Pal, A.K., Dalal, V., Batra, K., Sharma, T.R., Mohapatra, T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spermatophyta; Magnoliophyta; Liliopsida; Poales; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 176534)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 (Dases I to 176534)
3 (Dases I to 176534)
Swain, S.C., Sureshbabu, K., Singh, A., Pal, S., Gaikwad, K., Shazi, I.A., Dixit, A., Yadav, M., Srivastava, S., Bhargava, A., Pal, A.K., Dalal, V., Batra, K., Sharma, T.R., Mohapatra, T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (10-OCT-2002) IIRGS, NRC on Plant Biotechnology, Indian
Agricultural Research Institute, LBS Centre, New Delhi, Delhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Swain, S.C., Sureshbabu, K., Singh, A., Pal, S., Gaikwad, K., Ghazi, I.A., Dixit, A., Yadav, M., Srivastava, S., Bhargava, A., Pal, A.K., Dalal, V., Batra, K., Sharma, T.R., Mohapatra, T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomic sequence for Oryza sativa chromosome 11 Clone OSJNBa0070D14
                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (28-FEB-2003) IIRGS, NRC on Plant Biotechnology, Agricultural Research Institute, LBS Centre, New Delhi, De
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HTG; HTGS PHASE2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     singh, N.K.
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provided by the submittor.

This sequence will be replaced

by the finished sequence as soon as it is available and
the accession number will be preserved.

1 49567: contig of 49567 bp in length
                                                                                                                                                             n Feb 28, 2003 this sequence version replaced gi:27502456. NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have
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GSAPINLSDRLNQVLRWALGSVEILFSRHCPIWYGYGGRLKFLERFAYINTTIYPLTS
IPLLLYCILPAICLLTGKFIIPEISNFASIWFISLFLSIFATGILEMRWSGVGIDEWW
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REAMCFLMDPNIGRRVCYVQFPQRFDGIDRNDRYANRNTVFFDINLRGLDGLQGFVYV
GTGCVPNRTALYGYBEPIKKOKREGYFSSICGGRKKTKKKSKEKSTEKKKEHKHVDSSV
VFNLEDIEEGIEGSGFDDEKSLLMSQMSLEKRFGQSSVFVASTLMEYGGVPQSATPES
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complement(21685. .24525)
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IPPTTILIINLVGVVAGISYAINSGYQSWGPLFGKLFFAFWVIVHLYPFLKGLMGKQN
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/note="similar to polygalacturonase precursor GB:AC26512
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Pred. No. 1.5e+02;
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REFERENCE AUTHORS

TITLE JOURNAL REFERENCE

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TITLE JOURNAL

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ACCESSION VERSION KEYWORDS

RESULT 4 AC135242

DEFINITION

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Best Local Similarity
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                                sequence clones from Drosophila Gene Collection 1 (Rubin et al., Science 2000). The sequence has been subjected to integrity checks for sequence accuracy, presence of a polyA tail and contiguity within 100 kb in the genome. Thus we believe the sequence to reflect accurately this particular cDNA clone. However, there are arrifacts associated with the generation of cDNA clones that may have not been detected in our initial analyses such as internal priming, priming from contaminating genomic DNA, retained introns due to reverse transcription of unspliced precursor RNAs, and reverse transcription of unspliced precursor RNAs, and reverse transcription shout this sequence, including its location and relationship to other sequences, please visit our Web site (http://fruitfly.berkeley.edu) or send email to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta,
Neoptera, Endopterygota, Diptera, Brachycera, Musco
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                               Lawrence Berkeley National Laboratory, One Cyclotron Berkeley, CA 94720, USA Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Berkeley, CA 94720
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Drosophila melanogaster GH12788
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                      cdna@fruitfly.berkeley.edu.
                                                                                                                                                                                                                                                                                                                                                                This clone was sequenced as part of a high-throughput process to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (08-OCT-2001) Berkeley Drosophila Genome Project,
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/note="(japonica cultivar-group)"
38483 c 37230 g 49875 t 576 others
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/mol type="genomic DNA"
/db_xref="taxon:39947"
/chromosome="11"
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Location/Qualifiers
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97492: contig of 47825 bp in length
97592: gap of unknown length
145324: contig of 47732 bp in length
145424: gap of unknown length
148804: contig of 3380 bp in length
148904: gap of unknown length
165731: contig of 16827 bp in length
165831: gap of unknown length
165834: contig of 10703 bp in length.
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NOTICE: This sequence may not be the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between
                                                                                                             MAPPING: Clones were assigned to the YAC map by hybridization by M. Lodhi, Cold Spring Harbor Laboratories, and fingerprinted by M. Marra, Washu, to pick the best candidates for sequencing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana BAC F21B23.
AF262038
AF262038.1 GI:9502148
                                                                                                                                                                                                                                                                                                                      University,
Submitted by
                                                                                                                                                                                                                                                                                                                                         Submitted (01-MAY-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (thale cress) 
Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                 Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
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Washington University Genome Sequencing Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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/db_xref="GI:16182836"
/db_xref="GI:16182836"
/db_xref="GI:16182836"
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/translation="MIARRIVKELLIQEVPAQRDYELPEDSDWCAQEKLPPDTLCKLD
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EFSLGSDKRDNVKMMALCDLAMYIIDSKCLRFILEPLMAKRETFMFLAPEMYKEPAVANF
QNNDVYIFLDVYTLGAKSTSKAAATAMTTSRAAVAFKRPAEQSIMDDENPQENNLFDN
IRAADTTEPMAKRTRAGAASAKS"
IRAADTTEPMAKRTRAGAASAKS"
                                                                                                                                                                                                                             Department of Genetics, Washington University, St. Louis, MO 63108, USA e-mail: rwilson@watson.wustl.edu
                                                                                                                                                                                                                                                                                               Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="y; cn bw sp"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
/product="GH12788p"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="CG17509"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 map="48E2-48E2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Drosophila melanogaster"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene="CG17509"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="alignment with genomic scaffold AE003823"
db_xref="FLYBASE:FBgn0033676"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="Longest ORF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     390 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71284 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA
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neighboring submissions.
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This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one m13 subclone.

## NOTES:

Coding sequences below are predicted from computer analysis, using the program Genefinder(P. Green and L. Hillier, ms in preparation) 'ocation/Qualifiers

gene CDS SdC gene source /gene="F21823.3"
/gene="F21823.3"
20in(2429. 2626.2668. 2775,3508. 3920,4187. 4538,4709. 4932,5136. 5331,5530. 5597,5670. 5844,5931.
6028. 6081,6258. 6437,6567. 6679,6803. 6985,7177.
7456. 7515,7615. 7656,7752. 7879,7977. 8112,8243.
8454. 8570,8662. 8724,8808. 8909) SSHKKSSLDKSSSFKEQSPHVASVKSILESHASYLMSGKELSKLVAFVKGTQFDIVNF AAGLELIGQKLQMSELQNRLDAEFLLAQMCSVKFKEWIVVLATLLQRSEVLYDIFRYD LRLWKAYSVTLESHLAFAHYIDLLQILEAKLSATSREESNRGSIS" PLGILLPNVGVVVGVSQRMSFSASAEFACFEPTPQAQTILHCILRHILQRDKNEEALLL AQLSAEKHFSHCILBWLFTVDAEISRDNDRNNRQISGPGHLKKUSLLERKACDLIKKF PEYYDVVNVARKTDARHWADLFSAAGISTTILFEDCFQRRWYRTAACYYLIVIAKLGSV AVSQYCALRLLQATLDESLYDLAGELVRFILRSGRDIEQAPTESDSLSPKLLGFIIFG RFKKMRVFGDVSQEQQIHCKGLLMLGKIVVICNYIEASETYELLFYPRYHLDQSSLLC RKVLLGKMVMDVYQDYILVSYLFFFHYHVXIYGELFPSKADLQHLREGELDNDN LSSDLSDREPSRCLLIKGNGELSLLDLDVDGRERELTDSVELFMVTCGQSEEKIYNLVEE USMLDYGHRGMQGCPAPKCLTVTLYLIPVMYPSLGDDPFMQEDFLQLDPELEFDREVY KLLFVLNSDGQLVVCSVNKKGLKYTESIRAEKKVGGDAVCASVASEQQILAVGTRKGM VELYDLSHSISLLRTVSLHDWGYSADYTGPVNNIAWTEDNSAFAVGWKSBGLAVWSVS GCRLWSTVRQIGLTETSSEPKLIDKQDCKYEPLWSGTSALQWDBYGYRLFATEBASVE ILAFSFGKCCLNRGVSGKTYVRQVSYISQNWPVQHVAASEDGKYLAVAGLHGLILYDI /translation="mymaygwpqvipllpgscpssqrvvylklagrillvvspshlei wgssqvlyhhlsafpsnwsleiqrvrigkymrddksvreegeniqavwspdakiiavl fggafsigshpsdsnddrlisytlgnglvsgvasptlasddkfstnpaivqleictrs complement(join(10977. .11226,11408.
/gene="F21B23.5" complement(10977. .11830)
/gene="F21823.5" /note="contains similarity to Drosophila melanogaster BcDNA.GH03694 (GB:AAD55412); coded for by A. thaliana cDNA N96846; coded for by A. thaliana cDNA N96846; coded for by /protein\_id="AAF88009.1" /db\_xref="GI:9502156" db\_xref="taxon:3702" /mol\_type="genomic D
/cultivar="Columbia" organism="Arabidopsis chromosome="V" thaliana cDNA AA651310" one="F21B23" .11588,11647. .11830)) .5978, .7234, .8278,

Sgo gene

/gene="F21B23.6"

QGVIQMGLAENQVRLLIIYFIVICFQLCSDLIKEWIKENPHASICTAEGIDSFSDIAV FQDYHGLKQFRQVFISFLIRTIICFQIMFCLGTENKQAIATFMERARGGRVRFEAERV

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/evidence=not\_experimental /protein\_id="AAF88004.1"

note="contains

similarity

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aminocyclopropanecarboxylate

codon\_start=1

db\_xref="GI:9502151"

VMSGGATGANETIMFCLADPGDAFLVPTPYYAAYVYIHTLLVFK"

16686)

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/note="similar to a large family of Arabidopsis thaliana salt inducible protein-like proteins; contains similarity to Pfam family PF01535 (Domain of unknown function), score=340.5, E=1.9e-98, N=2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="mVDSGFPEHEIAASDKEKVSNLVPLVPTHGIIQSSEAEYCGICS
NPIFTVYLDSYGNVAKVEVDEDEVLSRRSGLDDLELVSSRLQKVLEDQMFKFALLIGL
GRQKIMREKEPGDGKGYPFVTFRCHDLAAEAIDNLNNVTPREPQNMGRNRGFAFIEYY
NHVKALYIKNLPRDITQERLKALFEHHGKIIKVVIPPAKVFREPQNMGRNRGFAFIEYY
MRALKNTERYEIDGHAAGGMSMMPIMLPDGRIRYVLQQPGLAAMPQPPPRPSPPYRGG
SGSSSKQSSDNGRGKSRYNPY"
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LINTILCKSRYDEALEVFEQMRGKRTDDGNVIKADSIHFNTLIDGLCKVGRLKEAEEL
LYRNKLEERCYPNAVTYNCLIDGYCRAKLEFAKEVVSRMKEDEIKPNVVTVNTIVGG
MCRHHGLNMAVVFFMDMEKEGVKGNVVTYMTLIHACCSVSNVEKAMYWYEKMLEAGCS
PDAKIYYALISGLCQVGRDHDAIRVPEKLKEGGFSLDLLAYNNLIGLFCDKNNEKVY
EMLTDDMEKEGKLOSTVTILISFFGGKHKDFSEVERMMEDGLDFTCHKNNEKVY
EMLTDDMEKGGKFDSITVTILSFKUNNEVINILIAPSKLKNEGGLDFTDKNAEKVY
AVGSVGELDEALKLFKDMGLHSKVNENTVINILIAAPSKLANGGLALSLKEEMKMKM
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AKSQSIKRRESSLSLALQSVIEFAGSEPDFRDKLLFLYEIAKEKNIPLTIVATKLLIR
WFGRMGNVAQSVLVYERLDSMKKASQVRNVVVDVLLRKGLVDDAFKVLDEMLQKESVE
PDNRITADIVLHEVWKERLLTEEKIIALISRFSSHGVSPNSVWLTRFISSLCKNARAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DGVSVYDPLEKIIPRWKGPSLDKNPEFLNNYHEQREALFSGKAASVSPVKYEEQSSHQ
ELSESASSENTLTPSSEITSSQPKIVVEGSDGSVRPGKKSGKEYWQHTKKWSRGFLEL
YNAETDPEVKAVMRDMGKDLDRWITEDEIKDAADIMEKLPERNKKFMEKKLNKLKREM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIPKLPAIGRALLFEYLIGLWILLKITLVVRKKSNEVECTELEKEMMRRKMKAWEERDMSE
KGTVEVLHKEGLEKPIMSFEKPKFDRNELMSSISKVKGSEKKIELVNSSHVEILDFDDK
IHEIKNMARRAREIEAGIELNEKEKRDVNKETGDSDEDISIGSGKSLEPIDGLTHSVGD
DDKDERLGTGTDSENTELSAFAVPMLNGAMVDSGFPNHEMAASDKKKVSNVVPLVPTD
GVIQASDVTKOQLSMMKNSTGRKSRVIRSVKBAKEFLSRRSGEKELTQELSQMAQDSD
EIFPKQSDEERGVARKHKLVDKNKILELYRSEYNDELEMMKDEKLRDIVFCVRDNELA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (27206. .29561)
/gene="F21B23.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="contains similarity to Pfam family PF00076 (RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)), score=42.1, E=1.3e-08, N=1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(join(24152. .24287,24374. .24440,24665. .24872,
25152. .25208,25625. .25735,26021. .26062,26667. .26942))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /evidence=not_experimental
/protein_id="AAF88005.1"
/db_xref="GI:9502152"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="contains similarity to Drosophila melanogasterspectrin beta chain (GB:AAA28399.1) and heparan sulfate-N-deacetylase/N-sulfotransferases"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VRPNVETYNALFKCLNEKTQGETLLKLMDEMVEHLVNQIRSQWRF"
Complement(24152. .26942)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="F21B23.6"
                                                                                                                                                                                                                                                                                                                                                                                                                               ELFGPQAVVS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /evidence=not_experimental
/protein_id="AAF88007.1"
/db_xref="GI:9502154"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (join (27206. .27759, 28027.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /evidence=not_experimental
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                                                                                                                                                                                                                                /gene="F21B23.2"
/gene="821B23.2"
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40816. .40861,40959. .41072,41156. .41317,41364. .41443)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene="F21B23.7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translation="MENGEYVTHKDTSLLKFVSSSSSSSEEEFRFVSSIQNAILRLD"
                                                                                                                                                  note="contains similarity to Pfam family PF00350 (Dynamin amily), score=29.7, E=4e-06, N=2"
                                                                                                                  codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     _start=1
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ORGANISM
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                                                               Genes were identified by a combination of several methods: Gene prediction programs including Genscan+ (Chris Burge, http://CCR-081.mit.edu/GENSCAN.html), GeneMarkHYM (Mark Borodovs http://genemark.biology.gatech.edu/GeneMark/), GlimmerA (a varie of GlimmerM, see Mihaela Pertea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 91268)
Town, C.D., Haas, B.J., Wu, D., Maiti, R., Hannick, L.I., Chan, A.P., Tallon, L.J., Rooney, T., Utterback, T.R., VanAken, S.E., Feldblyum, T.V., White, O. and Fraser, C.M.
Arabidopsis thaliana chromosome 2 BAC F23H14 genomic sequence
                                                                                                                                                                                                                                                                                                       Submitted (27-FEB-2002) The Institute for Genomic Research, Medical Center Dr. Rockville, MD 20850, USA, cdtown@tigr.or On Apr 18, 2002 this sequence version replaced gi:6598619.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
http://www.tigr.org/softlab/glimmerm_htm/glimmerm.html, and GeneSplicer (Mihaela Pertea and Steven Salzberg, contact mpertea@tigr.org), searches of the complete sequence agains
                                                                                                                                                                                                                                                                                                                                                                                            Medical Center Dr., R
3 (bases 1 to 91268)
Town, C.D. and Kaul, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (09-MAR-2000) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA
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                                                                                                                                                                                                                                                                                 Address all correspondence to:at@tigr.org
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
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                                                                                                                                                                                                               clone F23H14 is from Arabidopsis thaliana chromosome 2 orientation of the sequence is from SP6 to T7 end of the BAC
                                                                                                                                                                                                            orientation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence.
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57055. .59355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="mayvnkenaikmaeqnlkanseihkvslldevndrfmylsqara
naqlievlegggvlerekeqvdewlkdfadaevnlnrfmaelkddlkapafefaflsp
gghryvesladeagitdqagsllfakdnrfsebld"
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/gene="F21B23.9"
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/gene="F21B23.9"
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/protein_id="AAF88008.1"
/db_xref="GI:9502155"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="contains similarity"
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Pred. No. 3.3e+02;
0; Mismatches 2;
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BAC F23H14 genomic
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                                                                                                                                                                                                                                                                                                                               cdtown@tigr.org
                                                                                                                       (Mark Borodovsky,
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                                                                                                 (a variant
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spacer between 25S and 18S rDNAs"  1459. 1829  /rpt_family="Rf:rDNA repeat of 18S rDNA, intergenic spacer, 5.8S rDNA, spacer, 25S rDNA, spacer entire repeat unit is 10.5 kbp, 2 loci of ~3.5 Mbp on chromosomes II and	repeat"  repeat_region 449502  /rpt_family="Rf:Spacer between 25S and 18S rDNAs part of the 10.5 kbp rDNA repeat#Rf:ATR0032 X15550 intergenic	repeat_region 447500  470500  /rpt_family="Rf:rDNA repeat of 18S rDNA, intergenic pacer, 25S rDNA, spacer entire repeat on the spacer, 5.8S rDNA, spacer, 25S rDNA, spacer entire repeat unit is 10.5 kbp, 2 loci of -3.5 kbp on chromosomes II and IV, 670 copies#Rf:ATR0026 X52322 X15550 10.5 kbp rDNA	770 copies#Rf:AIR0026 X52322 X15550 10.5 kbp rDNA 1t" 1501 -501 -501 -501 -501 -501 -501 -501	repeat_region 412501  /rpt_family="Rf:Spacer between 25S and 18S rDNAs part of /rpt_family="Rf:Spacer between 25S and 18S rDNAs part of the 10.5 kbp rDNA repeat#Rf.ATR0032 X15550 intergenic spacer between 25S and 18S rDNAs rDNAs repeat_region 414503  /rpt_family="Rf:rDNA repeat of 18S rDNA, intergenic spacer; 25S rDNA, spacer entire repeat unit is 10.5 kbp, 2 loci of ~3.5 Mbp on chromosomes II and	the To.5 kbp rDNA repeat#Rf:ATR0032 X15550 intergenic spacer between 258 and 188 rDNAs"  repeat_region 852705 /rpt_family="Rf:rDNA repeat of 188 rDNA, intergenic spacer, 5.88 rDNA, spacer, 258 rDNA, spacer entire repeat unit is 10.5 kbp, 2 loci of ~3.5 Mbp on chromosomes II and IV, 670 copies#Rf:ATR0026 X52322 X15550 10.5 kbp rDNA	repeat_region 10.5 kbp rDNA repeat_region 0.5 kbp rDNA repeat_region 1. 85 the To.5 kbp rDNA repeat#Rf:ATR0026 X52322 X15550 10.5 kbp rDNA repeat#Rf:ATR0032 X15550 intergenic spacer between 25S and 18S rDNAs part of spacer between 25S and 18S rDNAs part of repeat_region 80. 2705  repeat_region 80. 2705	/db_xref="taxon:3702" /chromosome="2" /map="mi398" /clone="F23H14" misc_feature 1. 9372 /note="rDNA 10.5 kbp repeat unit" repeat_region 1. 88 repeat_region 1. 88 rDNA, spacer, 25 rDNA, spacer entire repeat unit is 10.5 kbp. 2 loci of -3.5 kbp. on chromosomes II and unit is 10.5 kbp. 2 loci of -3.5 kbp. 2	peptide database and the plant EST database at TIGR (http://www.tigr.org/tdb/tgi.shtml). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other protesins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats are identified by repeatmasker (Arian Smit, http://ftp.genome.washington.edu/RM/RepeatMasker.html).  FEATURES  1. 91268 /organism="Arabidopsis thaliana" /cultivar="Columbia"
" VAs pa	the 10.5 kbp rDNA repeat#Rf:ATM0030 [X52320] X52322 [U43225 intergenic spacer between 5.8S and 25S rDNAs" repeat_region 51348520 /rpt family="Rf:25S rDNA contained within the 10.5 kbp	repeat_region 4782. 4945 /rpt_family="Rf:5 88 rDNA contained with the 10.5 kbp rDNA /rpt_family="Rf:5 88 rDNA contained with the 10.5 kbp rDNA repeat_region 4946. 5133 repeat_region 4946. 5133 /rpt_family="Rf:Spacer_between 5.88 and 258 rDNAs part of	~ n.u.a ~ a ~ .	Yelle	reperator 2706 /rpt. space unit IV, reperator	/pt family="Rf:Spacer between 25S and 18S rDNAs part of the 10.5 kbp rDNA repeat#Rf:ATR0032 X15550 intergenic spacer between 25S and 18S rDNAs" repeat_region 2081. 2139  /rpt_family="Rf:rDNA repeat of 18S rDNA, intergenic spacer, 5.8S rDNA, spacer, 25S rDNA, spacer entire repeat unit is 10.5 kbp, 2 loci of -3.5 Mbp on chromosomes II and IV, 670 copies#Rf:ATR0026 X52322 X15550 10.5 kbp rDNA	/rpt f the Tio spacer 1771. /rpt f spacer unit i IV, 67 region 2079	.5 kbp rDNA rDNAs part intergenic rDNAs part intergenic intergenic rentire rep romosomes II

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VERSION
KEYWORDS
SOURCE
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AUTHORS
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NCB14A6/c
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (18-JAN-2002) MIPS, Institut fuer Bioinformatik, GSF-Forschungszentrum fuer Umwelt und Gesundheit, GmbH, Ingolstaedter Landstrasse 1, D-85764 Neuherberg, FRG, E-mail: G.Mannhaupt@gsf.de Project Coordinator: Ulrich Schulte, Institute of Biochemistry, Heinrich-Heine-University, D-40225 Duesseldorf, E-mail: ulrich-schulte@uni-duesseldorf.de this contig is an assembly of BAC 14A6 from 1 to: 11263, and BAC 12H4 from 11264 to: 91436rev (strain OR74A); BAC clones are available at the Fungal Genetic Stock Center http://www.fgsc.net sequencing was performed by MWG Biotech AG, Ebersberg, Germany,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neurospora crassa DNA linkage
AL670007
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora
                                                                                                                                                                                                                                                                                                                                                                    Information on performance of analysis and a more detailed annotation of this entry and other sequences of linkage groand V can be viewed at: http://mips.gsf.de/proj/neurospora.
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Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.mwgdna.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
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9195. .9372
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/rpt_family="Rf:rDNA, spacer, 25S rDNA, spacer entire repeat
spacer, 5.8S rDNA, spacer, 25S rDNA, spacer entire repeat
unit is 10.5 kbp, 2 loci of ~3.5 Mbp on chromosomes II and
IV, 670 copies#Rf:ATR0026|X52322|X15550 10.5 kbp rDNA
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spacer, 5.8S rDNA, spacer, 25S rDNA, spacer entire repeat
unit is 10.5 kbp, 2 loci of ~3.5 Mbp on chromosomes II and
IV, 670 copies#Rf:ATR0026|X52322|X15550 10.5 kbp rDNA
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9197. .9374
               complement (join (5919.
/gene="B14A6.010"
complement (join (5919.
                                                                                                                                                                    /note="overlap to BAC B1308 contig, entry for analysis and annotation"
                                                                                                                                                                                                                                                           organism="Neurospora crassa"
|mol_type="genomic DNA"
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                                                               'gene="B14A6.010"
                                                                                                    note="tRNA predict as a tRNA- Gln :
                                                                                                                           product="tRNA-Gln"
                                                                                                                                                                                                                                        chromosome="2"
                                                                                                                                                                                                                                                                                                                                                 ocation/Qualifiers
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90.0%;
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.6185,6494.
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  .7692,7761. .7803))
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KRAVEKSEAMNPSKPTKVEPETALPKVHVPTPQTARQKTAAADVEATKAGKVAAAA
QEEQAQMDQQQQQETQKPKKKEKKYAPEAMIPTSRFVGNVGKTAGAALDTTGQVA
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ITGGLGDGVGKIGQDDLGGVGDVTGGVTNGVGGLLGGVLGGGGGGQRR"
complement (5919...6185)
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IPAQRRAMTPSDTPSVSAALAILDWRRKAQTPTSNTSAATEPVLVTRRPSNSFRPMDS
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LDALGIHAPFGRVYATSIAPTDGRYKGSACALITMFCREEAVHVFQFTTGGNLKIAGR
TIAVWNSNRSAPQTTDLPHSASRVLEILGPIEVVDIHRLSRFLGANIKFDTQDVTTVR
EDKDERLLRWTFCSFRAQAQVARKALRAEWPGLHIRWGIDPMAVSVNNVPTAMSTMLP
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/gene="B14A6.010"
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contains EST gb:AW717407, AW708782"
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/gene="B14A6.010"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contains ATP/GTP-binding site motif A (P-loop)
DFYDAFVSTRÄGLENTRÖRAEHTRKRKTVSHTFSAKSVQQFEPYMHSNLELFVKQWDS
MIKNSKNPDKAAHLDCLEWFNYLAFDVIGDLSFGQPFGMLSSGADMAEIRSSPDAAPI
YAPAIEILNRRGEVSATLGIHPALKPFAKYLPDPFFTKGLAAVENLAGIAIACVKSRL
                                                                                       /protein_id="CAD21305.1"
/bb_xref="GI:18376189"
/ta=nslation="MAIISILMSPWAPVVLLAGVAFYYLVPYFVTYSALRKIPSPFPA
QFTDLWLLSVCRRGNRYQRVDELHKKLGPVVRIQPNHVSICDDAAIFTIYGHGNGFLN
                                                                                                                                                                                                                                                                                                                                     /note="strong similarity to benzoate 4-monooxygenase (EC 1.14.13.12), Aspergillus niger, PIR:S12015 Contains Cytochrome P450 cysteine heme-iron ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join(13804 .15031,15093 .15397))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (join (13804.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13287. .13358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
/product="hypothetical protein"
/protein_id="CAD21304.1"
/db_xref="GI:18376188"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="B14A6.010"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene="B14A6.010"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        number=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'gene="B14A6.010"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    product="putative protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="match of 76 ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13804. .15397
/gene="B14A6.030"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LFPQQRAPVATSEVSHTPAGDLISFDSDVEEGLDSKEEKSDIYDF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'gene="B14A6.020"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             number=1
                                                                                                                                                                                                                                                                                                              signature [FSHGPRSCVG] "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       product="tRNA-Thr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene="B14A6.020"
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                                                                                                                                                                                                                                                                                                                                                                                                                                      gene="B14A6.030"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               number=:
                                                                                                                                                                                                                                              product="probable benzoate 4-monooxygenase
                                                                                                                                                                                                                                                                                 codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene="B14A6.030"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="tRNA predict as a tRNA- Thr : anticodon agt"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    number=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .7803)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .7692)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .7760)
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/gene="B14A6.040"
complement(17314. .19917)
/gene="B14A6.040"
complement(17314. .19917)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="CAD21307.1"
/db_xref="G1:18376191"
/db_xref="G1:18376191"
/translation="MSLAKVKHIVLVL/SGKGGVGKSSVTTQLALSLSLAGHSVGVLDV
/translation="MSLAKVKHIVLVL/SGKGGVGKSSVTTQLALSLSLAGHSVGVLDV
DLTGPSIPRMFGIEDAKVTQAFGGWLFITVHEADPSAGYGSLRYMSLGFLLPKKGDAV
VWRGPKKTAMVRQFLSDVFWDETDYLLIDTPFGTSDEHISLAENLLQKARPGQLAGAV
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RSTSPSDDTTHGDERQDSP1TSIDDSHARPRLAKKSSSIVQKEVEEPKTAQVWSQ
RSTSPSDDTTHGDERQDSP1TSIDDDSHARPRLAKKSSSIVGKEVEEPKTAQVWSQ
GPPVLRRAESKSSLGPHHHDVSEEASDFGDFEDAQVKEPPSSQTPEPESTPSEVQKPS
SQHGSSPTTSPTQSMSSQLGHMNELAAKFGALNFDIDLSNVDKMFETSTNMKPLFPYA
                                                                                                                                                                                                        20645. .20730
/gene="B14A6.050"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="similarity to putative nucleotide binding protein, Homo sapiens, TREMBL:AF118394_1 Contains ATP/GTP-binding site motif A (P-loop) [GKGGVGKS]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="B14A6.050"
join(20612..20644,20731..21612)
/gene="B14A6.050"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (17314.
/gene="B14A6.040"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPVSTLTSTRGPNPGTTTAEYMSQSDHVPVSLTLTSNLENNTTVPVTSSAADPWASAD
FSFFELPSQQQIGPTKSSVTPSRPSSMIATSFAPTAPGSSTHSFDLPRVTTPISSASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DVSDHIITDSFNSISERKAMYRISRFGSSRKHNAGDDENYRRVAMPTSTVCQETLQTV
RRMKEEDSIAGRVSLGGGISKTQKNMFGWDSSAEPVTLDAIFGKRAVPTRESSVQDLQ
PESAENLVDHSEPLGGTAVUSLKWQBHRPASLGLPPAATFSWSSDPSASAKEPLTASL
PLTPSQPAQGPFKVTPMDLGMSSISATAAAEDNDDDWGEMVSSPSVTKATVGGFPDFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LPAITAPSPWADAEDGFGGWAAPDGLTTQTATTAQSAWMGGWRSRSPSLAAPSRDNGF
RSRSPSLVAPSRENSWRSRSPSLIAPSRDNGFRSRSPSLAASVRDEEFAKSNPIAWPD
TIASSNSPIAPVLRQPSPDFWAAEHSHTPHNDDNITPRLVINLPQSIAEEEDDVDKGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jompy entercation (C.C.)
/gene="B146.040"
/note="similarity to glucan 1, 4-alpha-glucosidase (EC /note="similarity to glucosidase (EC /note="similari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="B14A6.030"
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HDASQGVH1QGYYLPPGTVLSVPTYS IHHSKEIWGPDADEFKPERMERLTARQKNAFI
PPSHGPRSCVGRNVAEMEMKLI VATWARRYEVKLLQDYMDTREGFLRKPLGLKVGLKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VVTTPQAVATADVRKELNFCTKTN1RVL/GVVENMCGFVCPNCSECTN1FMSGGGEVMA
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                                            /gene="B14A6.050"
                                                                                                                                                                 'number=
                                                                                                                                                                                                                                                                                                                                                                   gene="B14A6.050"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RLVHKYKDCSLAPIFSKITADVISAVQQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NDFGVRFLGRVPIDPQFLVLIETGKRPTYPAGTTVDGKDISTPAGASTSEEEEVKDGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          product="related to putative nucleotide binding protein
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protein_id="CAD21306.1"
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number=2
                                                                                                                                                                                                                                                                                                                       number=
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REFERENCE
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATAC010927/c
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                  http://gnomic.stanford.edu/~chris/GENSCANW.html), and NetPlantGene (http://www.cbs.dtu.dk/netpgene/cbsnetpgene.html). searches of the complete sequence against a peptide database and the Arabidopsis EST database at TIGR (http://www.tigr.org/tdb/at/at.html). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://dx.database.com/server/add/.database.com/server/add/.database.com/server/add/.database.com/server/add/.database.com/server/add/.database.com/server/add/.database.com/server/add/.database.com/server/add/.database.com/server/add/.database.com/server/add/.database.com/server/add/.database.com/server/add/.database.com/server/add/.database.com/server/add/.database.com/server/add/.database.com/server/add/.database.com/server/add/.database.com/server/add/.database.com/server/add/.database.com/server/add/.database.com/server/add/.database.com/server/add/.database.com/server/add/.database.com/server/add/.database.com/server/add/.database.com/server/add/.database.com/server/add/.database.com/server/add/.database.com/server/add/.database.com/server/add/.database.com/server/add/.database.com/server/add/.database.com/server/add/.database.com/server/add/.database.com/server/add/.database.com/server/add/.database.com/server/add/.database.com/server/add/.database.com/server/add/.database.com/server/add/.database.com/server/add/.database.com/server/add/.database.com/server/add/.database.com/server/add/.database.com/server/add/.database.com/server/add/.database.com/server/add/.database.com/server/add/.database.com/server/add/.database.com/server/add/.database.com/server/add/.database.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (24-JAN-2001) The Institute for Genomic Research, Medical Center Dr., Rockville, MD 20850, USA On Jan 24, 2001 this sequence version replaced gi:12280869. Address all correspondence to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (28-SEP-1999) The In Medical Center Dr. Rockville, 3 (bases 1 to 96232)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complete sequence.
AC010927
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genes were identified by a combination of three methods: Gene prediction programs including GRAIL (available by anonymous ftp from arthur.epm.ornl.gov). Genefinder (Phil Green, University o Washington), Genscan (Chris Burge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BAC clone T22K18 is from Arabidopsis chromosome III and is near the molecular marker CIC5D8.

The orientation of the sequence is from SP6 to T7 end of the BAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ronning, C.M., Koo, H., Fujii, C.Y., Utterback, T.R., Barnstead, M.E Bowman, C.L., White, O., Nierman, W.C. and Fraser, C.M. Arabidopsis thaliana chromosome III BAC T22K18 genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 96232)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e-mail: xlin@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The Institute for Genomic Research
9712 Medical Center Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
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http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats are
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lin, X
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/note="identical to TREMBL:AF151380
Contains Fumarate lyases signature
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23875. .25386
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90.0%;
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Pred. No. 3.
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,C.Y., Utterback,T.R., Barnstead,M.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Institute for Genomic Research,
, MD 20850, USA, xlin@tigr.org
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              identified by repeatmasker (Arian Smit,
                                                                                                                                                                                                                                                                         /proteIn_id="AAF04409.1"
/db_xref="G1:6143862"
/translation="MKKPSLFQ1!IIVLSIPTTTGRTVGNLRVREGSPFKIAIFADLH
/GEDTWTDWGPGQDVNSVNVMSAVLDAETPDFVVYLGDVVTANNIAIQNASLFWDKAI
SPTRDRGIPMATLFGNHDDASFYWPLDWLSSSGIPPLRCPAASDDDGCTFRGTTRVEL
IQEEIKSSNALSYSMISPKELWPSVSNYVLLVESSDHSKPPVALLYFLDSGGGSYPEV
ISNAQVEWFKTKSNTLNPYLRIPELIFWHIPSKAYKKVAPRLMITKPCVGSINNEKVV
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1880. .1926,2058. .2148,2480. .2619,2713. .2955,3152. .3
3312. .3467,3548. .3744,3890. .3949)
/gene="T22K18.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GB:AAA87568 [Homo sapiens]"
join(<877. 929,1009. 11069,1403. .1486,1588. .1644,
1737. .1797,1880. .1926,2058. .2148,2480. .2619,2713.
3152. .3230,3312. .3467,3548. .3744,3890. .>3949)
/gene="T22K18.1"
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STAILLENCMEVRDPQVLLPKLVTTCASSGTHFSRALFVPSMSTVNKVISGASALPSD
TRRKDLTWQFELQRLMEKSIQGTDAGLDHTLKEDGITALPEHDFLCGDAPQCGGPAGT
PVTSSAVMPSLPLTINWLRDCVRRNPSLKLEVLVTGSLHLVGDVLRLLKR"
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ltmpplfQtltvlafklfvcfkvdvavlevglogkldstnviqkpvvcgtaslcamdh
ddilantladiafkhqoiffkyddavlevkldstndvldktbvtvaphlekkkld
GVTLGLSGDHQLvnaglavslsrcwlqrtgnwkkifpnesketeipvafcrglatarl
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complement (437. .495)
Tocte="similar to RecA protein GB:BAA78779
[Rhodopseudomonas palustris]"
complement (join (6468. 6744, 6877. .7016, 7118. .7264, 7342. .7514, 7741. .7828, 7938. .8155, 8232. .8295, 8491.
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                                                                                                                                    /note="exon predicted by xgrail, quality good_shadowexon"
complement(<6468. .>8553)
                                                                                                                                                                                               complement (6053.
                                                                                                                                                                                                                            SRILEISEMPFRIKTWIRMEDGSVHSEVNLTYD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="predicted by genscan+"
join(<4481. .4703,4985. .5477,5564.
/gene="T22X18.2"
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/note="similar to folylpolyglutamate synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="exon predicted by xgrail,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="overlap with BAC clone F14P13
(AC009400:87230. .87937)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /chromosome="III"
/map="CIC5D8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultivar="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                     AQEAENGMMRVLENRSSVKAVFVGHNHGLDWCCPYKDKLWLCFARHTGYGGYGNWPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               join(4481. .4703,4985. .5477,5564.
/gene="T22K18.2"
/note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="exon predicted by xgrail, quality marginal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'product="putative folylpolyglutamate synthetase"
'protein id="AAF04408.1"
'db_xref="GI:6143861"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone="T22K18"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene="T22K18.2"
                                                                                                                                                                                                     .6230)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           quality good_shadowexon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .5732,5817. .6035)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .5732,5817. .>6035)
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           .>8553))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NLDLALGVGGLPKGRMVEVYGKEASGKTTLALHI IKBAQKLGGYCAYLDAENAMDPSL
AESIGVNTEELLI SRPSSAERMLNI VDVLTKSGSVDVI VVDSVAALAPQCELDAPVGE
RYRDTOGRALMYDALKKIHYSVGYSGYLI VFLNQVRSHVKSINMIFPHAEEVTCGGNALP
FHAAIRLMIRTGLI KTANKVYGLNVCVQVVKNKLAPGKKKSELGIIFGHGFYVEREV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAEYLFGKNTIKEKMEMTTPVVTRKVQSVGEKMEMTTPVITSKAKDQNQWRMSFVMPS
KYGSNLPLPKDPSVKIQQVPRKIVAVVAFSGYVTDEEIERRELRRALQNDKKFRVR
DGVSEEVAQXNPPFTLPFMRRNEVSLEVENKED"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="mmmissssitsslsllssspeklplinpiqrcpitysgfrtasv
NRAIRRQPQSPAVSATESRVSLVLALASQASSVSQRLLADLAMETAKYVFPKRFDSST
NLEEAFMSVPDLETMNFRVLFRTDKYEIRQVEPYFVAETIMPGETGFDSYGASKSFNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="exon predicted by xgrail, marginal shadowexon"
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7342. .7514,7741. .7828,7938. .8155,8232. .8295,8491.
/gene="T22K18.3"
        /note="exon predicted by xgrail, complement(14089. .14181)
/note="exon predicted by xgrail,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (9461. .9610)
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ASDCELDEVPDDRKVAEKDTALHLALSQLSGDFDKDSKLSLQRFYRKRRVSVISTGSL
                                                                                                                                                                                               complement (13084.
                                                                                                                                                                                                                                                                              /translation="MEKKVIKIMRNDGKVVEYRGPMKVHHILTQFSPHYSLFDSLTNN
CHLHPQAKLLCGRLYYLLPQETNSIKHMKKTMKKVRFANPEVEKEEQEEDRLTDCCDN
                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (12861. .13364)
/gene="T22K18.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="predicted by genscan+,
complement(12647. .13454)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (12647. .13454)
/gene="T22K18.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       marginal_shadowexon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (12526. .12557
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/db_xref="GI:6143864"
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/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         join(10379. .10619,10701. .10790,10871. .10941,11030. .11131,
11228. .11332,11695. .11830,12181. .12260,12341. .12415)
/gene="T22K18.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="predicted by genscan+, est match"

/oin(<1979, 10619,10701, 10790,10871, 10941,11030, 1

11228, 11332,11695, 11830,12151, 12260,12341, >12415)

/gene="T22K18.4"
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/protein_id="AAF04410.1"
/db_xref="GI:6143863"
                                                                                                                                                                                                                                                        TKEKTNGVVRVKMVVSKQELEKLLQGGSVHEMVYRTLAKQHLCDDDDECHKEGWRPLL
                                                                                                                                                                                                                                                                                                                                 /protein_id="AAF04412.1"
/db_xref="GI:6143865"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="T22K18.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="exon predicted by xgrail, quality"
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                                                                                                                                                                                                                                                                                                                                                                                                                   note="unknown protein"
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                                                                                                                                               family="(GAA)n"
[ement(1222]
                                                                                       family="(CAAA)n"
. .13970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          multiple est matches"
     quality marginal"
                                                              quality good_shadowexon"
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Length 173613;

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REFERENCE
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AC007475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Holt,R.A., Evans,C.A., Gocayne,J.D., Amanatides,P.G., Brandon,R.C., Rogers,Y., An,H., Baldwin,D., Banzon,J., Beeson,K.Y., Busam,D.A., Carlson,J.W., Center,A., Champe,M., Davenport,L.B., Dietz,S.M., Dodson,K., Dorsett,V., Doup,L.E., Doyle,C., Dreensk,D., Farfan,D., Ferriera,S., Frise,E., Galle,R.F., Garg,N.S., George,R.A., Gonzalez,M., Houck,J., Hoskins,R.A., Hostin,D., Howland,T.J., Ibegwam,C., Jalali,M., Kruse,D., Li,P., Mattei,B., Moshrefi,A., McIntosh,T.C., Moy,M., Murphy,B., Nelson,C., Nelson,K.A., Nunoo,J., Pacleb,J., Paragas,V., Park,S., Patel,S., Ffeiffer,B., Phouanenavong,S., Fitman,G.S., Purl,V., Richards,S., Scheeler,F., Stapleton,M., Strong,R., Svirskas,R., Tector,C., Williams,S.M., Zaveri,J.S., Smith,H.O., Rubin,G.M. and Venter,J.C. Sequencing of Drosophila chromosome 2R, region 49A-49B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Direct Submission
Submitted (05-MAY-1999) Drosophila Genome Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, B., Blazej, R.G., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E., Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
                                                                                                                                                                                                                                                                                                                              and relationship to other sequences, please visit ou: archive Web site (http://www.fruitfly.org/sequence/) to bdgp@fruitfly.berkeley.edu.
                                                                                                                                                                                                                                                                                                                                                                              This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
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AC007475.7 GI:13162478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (fruit
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/clone="BACR04E21 (D592)"
/clone lib="RPCI-98 (Roswell Park Cancer Institute
Drosophila melanogaster BAC library, partial EcoRI in
                                                                                                                                               /strain="y; cn bw sp"
/db_xref="taxon:7227"
                                                                                           chromosome="2R"
map="49A-49B"
                                                                                                                                                                                                                                           organism="Drosophila melanogaster"
                                                                                                                                                                                                                                                                                                     ocation/Qualifiers
                                                                                                                                                                                                               mol_type="genomic DNA"
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90.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     173613 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       replaced gi:6957978
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د (۵)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INV 28-FEB-2001
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AC007474
LOCUS
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ORIGIN
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Best Local
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Rolt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C.,
Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A.,
Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M.,
Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D.,
Ferriera, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A.,
Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J.,
Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattel, B., Moshrefi, A.,
McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunoo, J.,
Pacleb, J., Paragas, V., Park, S., Patel, S., Patel, S.,
Phouannavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F.,
Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M.,
Zaveri, J.S., Smith, H.O., Rubin, G.M., and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25802
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BACR14L19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Celniker, S.E. Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G. Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J. M., Park, S., Pfeiffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E., Pfeiffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E., Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
                                                                                                                                                                                                      This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (05-MAY-1999) Drosophila Genome Center, Lawrence Laboratory, MS 64-121, Berkeley, CA 94720, USA On Feb 28, 2001 this sequence version replaced gi:5670617.
                                                                                                                                                                                                                                                                                                                                                                                                                Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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1 (bases 1 to 192763)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                        Berkeley, CA 94720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence submitted by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rubin, G.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequencing of Drosophila chromosome 2R, region 49A-49B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (fruit
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                                                                                                                                                                              Location/Qualifiers
                                 /strain="y; cn bw sp'
/db_xref="taxon:7227"
                                                                                           mol_type="genomic
                                                                                                                    organism="Drosophila melanogaster"
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90.0%;
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Pred. No. 3.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
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                REFERENCE
AUTHORS
                                                                                                                   KEYWORDS
SOURCE
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                         58864 CTGATGGCCAAACGAGAAAC 58845
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTG; HTGS_PHASE2.

Drosophila melanogaster

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 194634)

Adams, M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CTGATCGCCAAACGAGCAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission Submitted (30-DEC-1999) Celera Genomics, 45 West Gude Drive, Submitted, MD, USA Rockville, MD, USA This sequence was identified as CDM:10212663 by the submitter. For more information on this record e-mail to fly@celera.com.
                                                                                                                                                                                                                                                                                                                                         1 CTGATCGCCAAACGAGCAAC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC020286.1 GI:6664611
                                                                                                                                                                           206/32 bp DNA Rattus norvegicus clone CH230-334A14, '***, 2 unordered pieces.
                                                                                                                   AC109049
AC109049.4 GI:23101194
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Allen,C., Allen,H., Alsbrooks,S., Amin,A., A
                                                                Eukaryota; Mētazoa; Chordata; Craniata; Vertebrata; i
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                  Rattus norvegicus
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                                                 Rattus
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This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
                                (bases 1 to 206732)
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                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="BACR14L19 (D591)"
/clone lib="RPCI-98 (Roswell Park Cancer Institute Drosophila melanogaster BAC library, partial EcoRI pBACe3.6)"
a 41459 c 42141 g 54658 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                               þ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
42412 c 41301 g 55144 t
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90.0%;
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Pred. No. 3.5e+02;
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er, ***
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                                                                                                                                                                                                                                                                                                                                                                                           Score 16.8; DB 2; Length 194634; Pred. No. 3.5e+02;
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SEQUENCING IN
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                                                                                                                                                                                                                           linear
     Anguiano
       Adams,C., Alder,J.,
nguiano,D.,
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                                                                                                                                                                                                             HTG 09-OCT-2002
G IN PROGRESS
                                                                                         Euteleostomi;
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Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranike, D., Barber, M., Barnstead, M., Benhmed, F., Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bershmed, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bershmed, F., Biswal, K., Blair, J., Blankenburg, K., Calver, R., Chen, Y., Chacko, J., Chen, K., Cavazos, I., Ceasar, H., Center, A., D'Souza, L., Chacko, J., Jacko, J.
Direct Submission

Direct Submission

Direct Submission

Submitted (09-CCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Baylor Plaza, Houston, TX 77030, USA

On Sep 19, 2002 this sequence version replaced gi:21737800.

On Sep 19, 2002 this sequence combination of BAC based reads rhe sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas and whole genome shotgun sequencing reads assembled using Atlas in the feature table below represents a scaffold in the Atlas in the feature table below represents a scaffold in the Atlas in the feature table below represents a scaffold in the Requence assembly (a 'contig-scaffold'). Within each contig-scaffold, assembly (a 'contig-scaffold'). Within each contig-scaffold, assembly (a 'contig-scaffold'). Within each contig-scaffold with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence may extend beyond the ends of the clone and there may be sequence sontigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (03-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 (bases 1 to 206732)
Rat Genome Sequencing Consortium.
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REFERENCE AUTHORS TITLE

JOURNAL

TITLE

JOURNAL

REFERENCE

COMMENT

JOURNAL AUTHORS

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VERSION
KEYWORDS
                                                                                                                                                                                           RESULT 14
AC102969
                                                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
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Best Local Similarity
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                                                                                                               AC102969
Rattus norvegicus clone CH230-94M19,
***, 5 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                  18;
                                                   AC102969.7 GI:30522593
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED
Rattus norvegicus (Norway rat)
                                     Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                        CTGATCACCAAACCAGCAAC 65515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 2 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                        CTGATCGCCAAACGAGCAAC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                                                                                                                                                                                                                                                               54264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Baylor College of Medicine
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                                                                                                                                                                                                                                                                                                                                                                                                                                         end_sequence:RXAPN07TJ"
1 40169 c 41232 g 52474 t 18593 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     site:MboI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="wgs_contig"
complement(200587.
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site:MboI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="clone_boundary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="clone_boundary
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Pred. No. 3.5e
0; Mismatches
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                                                                                                                                           DNA
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TITLE
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Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 10, 2003 this sequence version replaced gi:24819627.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence
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Muzny, D. Marie., Metzker, M.Lee., Abramzon, S., Adams, C.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden,
Anyalebechi, V., Aoyagi, A., Barber, M., Barnstead, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (24-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 259345)
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Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rat Genome Sequencing Consortium.
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FEATURES
                                                                    RESULT -15
AC103330
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                          DEFINITION
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Best Local Similarity
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                     AC103330 261157 bp DNA linear HTG 13-MAY-2003 Rattus norvegicus clone CH230-177K18, WORKING DRAFT SEQUENCE, 7
unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_dainotte: This sequence may represent more than one clone. NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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Center clone name: CH230-94M19

Center clone name: CH230-94M19

Center clone name: CH230-94M19

Center clone name: Atlae 3.0;

Assembly program: Atlae 3.0;

Consensus quality: 242269 bases at least Q40

Consensus quality: 247151 bases at least Q30

Consensus quality: 24910 bases at least Q20

Estimated insert size: 260613; sum-of-contigs estimation quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         248467
248567
254508
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                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   /note="wgs_end_extension
clone_end:T7"
1 53670 c 51512 g 6682'
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251214. .254507
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complement(245699.
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clone_end:T7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
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xref="taxon:10116"
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90.0%;
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Pred. No. 3.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus
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Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Mētazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Submitted (13-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On May 13, 2003 this sequence version replaced gi:22857506.
                                                                                                                                                                                       of Molecular and Human
Baylor Plaza, Houston,
3 (bases 1 to 261157)
                                                                                                                                                                                                                                                              Submitted (24-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One
                                                                                                                                                                                                                                                                                                                               Worley, K.C.
Direct Submission
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                                                                                                                                                               Rat Genome Sequencing Consortium.
                                                                                                                                       Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: This sequence may represent more than one clone. NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
                                                                                                                  66925
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center clone name: CH230-177K18
------ Summary Statistics
Assembly program: Atlas 3.0;
Consensus quality: 247708 bases at least Q40
Consensus quality: 250022 bases at least Q20
Consensus quality: 251023 bases at least Q20
Consensus quality: 251033 bases at least Q20
Estimated insert size: 259364; sum-of-contigs estimation
Quality coverage: 9x in Q20 bases; sum-of-contigs estimation
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242149
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Project Information
Center project name: GLAH
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Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
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246232. .247626
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239309. .242048
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5033. .6658
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/clone="CH230-177K18"
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60485 c 60256 g
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     Score 16.8; DB 2;
Pred. No. 3.5e+02;
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length
bp in length.
                                                                                                               8001 others
                            Length 261157;
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Search completed: February 12, 2004, 04:41:47 Job time : 591.854 secs

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen

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Minimum DB
Maximum DB
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No.
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                         Score
       16.8
16.8
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seq length: 2000000000
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1: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
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3: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
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Human alpha-2BAR g
Drosophila melanog
Drosophila melanog
Drosophila melanoge
Human GDP-mannose
Human GDP-mannose
Human lung antigen
Human tweety homol
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ABX51029	AAC10249	AAQ49414	ABL06846	AAS79164	ABL06346	AAS86718		AAS9417	AAV2120	ABL0188	AAX2056	ABL0184	AAS2995	ABL1433		ABL0188	ABL0253			AAC4110	AAC4552	ABQ4508	ABQ4508		ABQ4415		ABZ1421	ABZ6682	ABT19	ABT18	ABQ6565	ABQ9159	ABQ91	AAV3045	AAV304
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ovine E		Cytochrome	Drosophila	encc	sophila	encc	sophila	encc	chanc	sophi	mucl	Drosophila	an lu	Drosophila	Aspergillus	зорhi	зорһі	Enterococcus	sophi	pidop	gobic	Jonuc	gonuc	Oligonucleotide	Jonuc	Drosophila m	pidop	pidop	ergil	Aspergillus	Arabidopsis	capsulatus	capsulatus	Rhizobium	Rhizobium
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## ALIGNMENTS

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PR 110-A 17-APR-2000; 2000US-0551744 10-AUG-2000; 2000US-0636259 19-OCT-2000; 2000US-0692077 Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor; polymorphic site; allelic variant; cardiovascular disease; central nervous system disease; adenylyl cyclase; MAP kinase activity; phosphorylation; inositol phosphate; alpha-2BAR; PCR primer; ss. Human alpha-2BAR genotyping PCR primer 18-FEB-2002 (first entry) Liggett SB, Homo AAI99909; WO200179561-A2. 17-APR-2001; 2001WO-US12575 25-OCT-2001. (LIGG/) LIGGETT S B. (SMAL/) SMALL K M. sapiens. Small KM; SEQ ID ö 15.

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ABL22105
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                                  Venter
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11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila; developmental pharmaceutical; gene; ds.
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                                                                                     (PEKE ) PE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20 BP; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (a) obtaining a sample having a polynucleotide encoding alpha2A or alpha2C or fragment or complement of; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to genotyping an alpha-2B,
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                                                                                  CORP NY.
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                         Adams M,
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2000US-0614150.
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                         PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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lic site,
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e, comprising;
g an alpha-2B,
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Best Local
                                                              Claim 1; SEQ ID NO 17785; 21pp + Sequence Listing;
                                                                                              New isolated nucleic acid
genes from Drosophila and
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                                                                                                                                                                                     23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster genomic polynucleotide SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072)
                                                                                                                                                  Venter
                                                                                                                                                                                                                   23-MAR-2001;
                                                                                                                                                                                                                                         27-SEP-2001
                                                                                                                                                                                                                                                                             Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                            Drosophila;
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                                                                                                                                                                                                                                                            WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                   26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                      ABL22104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid
genes from Drosophila and
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                                                                                                                                                                                                                                                                                                          developmental
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                                                                                                                                                                                                                   2001WO-US09231
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                                                                                                                                              PWD,
                                                                                         detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                      biology; cell signalling;
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Pred. No. 5
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                                                                                                                                                                                                                                                                                                       insecticide;
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent: useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA

invention illing and

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RESULT 4
ABX25006/C
ID ABX25006 standard; cDNA; 277 BP
XX
AC ABX25006;
XX
DT 11-FEB-2003' (first entry)
DE 11-JUN-2001; 2001US-0878574.
DE 11-JUN-2001; 2001US-0878574.
DE 22-NOV-1996; 96US-0753233.
DE 22-NOV-1996; 99US-0333177.
DE 22-NOV-1996; 99
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Best Local (
      4,6-dehydratase (GM4,6D) peptide. The peptide is useful for identifying GM4,6D inhibitors GM4,6D inhibitors are useful for reducing inflammation in a mammalian subject and for treating or ameliorating diseases affected by the level of cellular fucosylation or diseases affected by the ucosylation of glycoconjugates. These diseases include arthritis, transplant rejection, asthma, sepsis, repertusion injury, stroke or infection. The GM4,6D peptide or a polynucleotide encoding it is also useful for manufacturing complex carbohydrates and as targets for screening small molecule antagonists of the activity of the enzyme. The polynucleotide is useful in developing an assay for defects in the enzyme, as well as in gene replacement therapy. Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; GDP-mannose 4,6-dehydratase; GM4,6D; gene; ss; inflammation; cellular fucosylation; glycoconjugate fucosylation; transplant rejection; arthritis; asthma; sepsis; reperfusion injury; stroke; infection; complex carbohydrate; gene replacement therapy; immunosuppressive; antiinflammatory; antiarthritic; antibacterial; cerebroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New composition comprising GDP-mannose 4,6-dehydratase (GM4,6D) peptide, for manufacturing complex carbohydrates, or as targets for screening GM4,6D antagonists for treating e.g. arthritis, or transp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence data for this patent did not form specification, but was obtained in electronic f
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(ABB57737-ABB72072)
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Matches 17
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03-DEC-1997;
09-SEP-1998;
                 The invention relates to a composition comprising a human GDP-mannose 4,6-dehydratase (GM4,6D) peptide. The peptide is useful for identifying GM4,6D inhibitors are useful for reducing inflammation in a mammalian subject and for treating or ameliorating diseases affected by the level of cellular fucosylation or diseases affected by the fucosylation of glycoconjugates. These diseases include arthritis, transplant rejection, asthma, sepsis, reperfusion injury, stroke or infection. The GM4,6D peptide or a polymucleotide encoding it is also useful for manufacturing complex carbohydrates and as targets for screening small molecule antagonists of the activity of the enzyme. The polymucleotide is useful in developing an assay for defects in the anzyme, as well as in gene replacement therapy. Sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sullivan
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Sequences AAS29931-AAS30164 represent genomic DNA molecules, which encode CC the lung antigen polypeptides of the invention. Lung antigen polypeptides CC and their associated polynucleotides are useful in the diagnosis, CC treatment and prevention of various types of disorders in e.g. humans, CC mice, rabbits, goats, horses, care gogs, chickens or sheep. A CC pathological condition can be determined by detecting the presence or absence of a mutation in a lung antigen polynucleotide. The treatable CC disorders include autoimmune diseases such as rheumatoid arthritis, CC chyperproliferative disorders such as neoplasms of the breast or liver, CC cardiovascular disorders such as cardiac arrest, cerebrovascular coular disorders such as cardiac arrest, cerebrovascular coular disorders such as cardiac arrest, viruses and fungi, CC orban's disease, infections caused by bacteria, viruses and fungi, CC premature labour and infertility, gastrointestinal disorders such as CC crohn's disease, renal disorders such as glomerulonephritis and CC respitatory disorders such as asthma and pleurisy. The polypeptides can also be used to aid wound healing, to prevent skin aging due to sunburn, CC to maintain organs before transplantation, to regenerate tissues and in CC chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities.

CC CC at figuration, but was obtained in electronic format directly from WIPO CC at figuration int/pub/published_pct_sequences.
        17.NOV-2000
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                20-MAR-2001
                               AAF22305;
                                            AAF22305 standard;
                                                                                                                                          Sequence 47999 BP; 11178 A; 12727 C; 12874 G; 11209 T; 11 other;
                                                                                                                                                                                                                                                  New human tweety homolog 2 polypeptides and polynucleotides, useful for producing an antigen-binding molecule that is immuno-interactive with the polypeptide or as diagnostic markers for cancers -
                                                                                                                                                                                                                                     Claim 10; Page 128-156; 176pp;
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                                                                                                                      Score 15.8;
Pred. No. 2.
                                                                                                                                                                                                                                     English
                                                                                                               Mismatches
                                                                                                                       .3e+02
                                                                                                                             DB 25;
                                                                                                                            Length 47999;
                                                                                                               Indels
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RESULT 9
ABN68569/c
ID ABN68569
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Best Local S
Matches 17
27-OCT-2000; 2000GB-0026333.
24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
                                                                                                                                                                                                                                                Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; gene; antiinflammatory; infection; vaccine; meningitis; gene therapy; ds.
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01-APR-1999;
18-MAY-1999;
13-SEP-1999;
                                                                                   29-OCT-2001;
                                                                                                                                02-MAY-2002
                                                                                                                                                                     WO200234771-A2
                                                                                                                                                                                                               Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                           Streptococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                          ABN68569;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1082138 BP; 348775 A; 194404 C; 195515 G; 343444 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a recombinant DNA construct of a plant (Arabidopsis thaliana) centromere. The constructs are useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells expressing selected proteins such as hormones, enzymes, interleukins, clotting factors, cytokines, antibodies, and growth factors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant DNA construct comprising a plant centromere, useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-SEP-1999;
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Similarity 89.5%;
17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; DNA; 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGTTCGCCAAGCGAGCAAC 734795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGATCGCCAAACGAGCAAC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 977-1388; 1449pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thaliana.
                                                                                 2001WO-GB04789
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99US-0153584.
99US-0154603.
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Pred. No. 2.8e+02;
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RESULT 10
AAV30458/c
ID AAV30458 standard; DNA; 534720 BP.
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Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to determine whether a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus/GBS (Streptococcus/GBS (Streptococcus/GBS (Streptococcus/GBS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (1), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by
    Sg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
                                                                                                                                                                                                                                                     Rhizobium ep
                                                                                                                                                                                                                                                                                                           Symbiosis; open reading frame; ORF; plasmid; vector; transportation; degradation; metabolism; host range; nitrogen fixation; nodulation;
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Tettelin H;
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                                                                                                                                                                                                                                                                                           legume; plant;
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INST GENOMIC RES
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                                                                                            /standard_name= "ORF K1"
/product= "Oligopeptide permease"
/note= "homologous to the OppC ges
418673..419680
                                                                                                                                                                                             Location/Qualifiers
417796..418671
                  /*tag= b
/standard_name= "ORF K2"
/product= "oligopeptide |
/note= "homologous to th
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Pred. No. 2.6e+02;
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                  de permease"
the OppD ger
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/*tag= q
/standard name= "
/gene= "fixC"
/product= "protei
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ystandard name= "ORF K10"
/product= "transposase homologue"
/note= "homologus to the Tnp gene
complement (433880..434110)
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/product= "transposase homologue"
complement (431296..432840)
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/note= "homologous to the GLUD1 gene"
complement (430538..431284)
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/product= "(semi)aldehyde dehydrogenase-like protein"
complement (426949..428028)
                                                                          /product= "protein required complement (438605..439912)
                                                                                                                                                      complement (438297..438590)
/*tag= p
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    biosynthesis"
complement (436460..438130)
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/standard name= "ORF K5"
/product="aminotransferase-like protein"
/ ייב מאריים וואר אונים אונים וואר אונים אונ
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complement (434517..434711)
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/product= "transposase homologue"
/note= "homologous to the Tnp gen
                                                                                                                                                                                                                                 /standard_name
/gene= "nlfA"
                                                                                                                                                                                                                                                                                                                                                  gene= "nIfB"
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/product= "ferrodoxin/ferrodoxin-like protein"
/note= "homologous to the FdxN gene"
complement (434753..436234)
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/product= "encapsulation-like protein"
/note= "homologous to the CapA gene"
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/standard_name= "ORF K3"
/product= "oligopeptide permease"
/note= "homologous to the OppF ge
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                                                                                                                                    name= "ORF K16"
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"protein required for nitrogenase activity"
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                                                                                                                                           /product= "protein involved biosynthesis" /note= "homologous to the Ni 457687..459096
                                 /note= "homologous to the FixF gene" 459093..459575
                                                                       /standard name= "ORF L7"
/gene= "nIfK"
/product= "beta-subunit
456187..457677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein"
/note= "homologous to the Lina 448497..450203
                                                                                                                                                                                                                                                                                                                                                 /product= "alpha-subunit of FeMo
154590..456131
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/product= "luciferase alpha-subunit-like protein"
/note= "homologous to the LuxA gene"
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/product= "gamma-hexachlorocyclohexane-dechlorinase-like
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/product= "protein of unknown
complement (443313...443879)
                                                                                                                                                                                                                                                                                                                                                                                          gene= "nifD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50341..451396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard_name= "ORF L3"
product= "putative protein with degradative function"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /standard_name= "ORF L1"

product= "cytochrome P450-like protein"

note= "homologous to the CamC gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= "protein required
complement (442316..442636)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= "protein required complement (441042..441899)
                                                                                                                                                                                                                                                                                                                                        *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              product= "C4-dicarboxylate transport protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /standard_name= "ORF K23"
/gene= "dctA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'etandard_name= "ORF K22"

'product= "ferrodoxin-like protein"

'note= "homologous to the NifQ gene"

145088..446602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note= "homologous to 46599..447843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44337..445029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard_name= "ORF K21"

product= "protein of unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /standard_name
/gene= "fixB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (439923..441032)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard
                                                                                                                                                                                                                         _name= "ORF L8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _name= "ORF K19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _name= "ORF K18"
                                                                                                                                                                                                                                                                                                                                                                                                          "ORF L6"
                                                                                                                                                                                                                                                                             of,
                                                                                                                                                             NifB gene'
                                                                                                                                                                                                                                                                           FeMo
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                                                                                                                                                                                                    FeMo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene"
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                                                                                                                                                                                                                                                                          protein
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                                                                                                                                                                                                    co-factor
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                                                                                                                                                                                                                                                                          nitrogenase
       RESULT 11
AAV30459/c
ID AAV304
XX AAV304
XX Symbio
DE Rhizob
XX Symbio
CKW degrad
KW 1egume
XX U09802
XX W09802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 16; Conserv
New isolated symbiotic plasmid from Rhizobium sp. NGR234 - develop products for modifying plant characteristics, e.g. fixation, synthesis of compounds and stress response
                                                                               WPI; 1998-110606/10
                                                                                                                                                       (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                         Symbiosis; open reading frame; ORF; plasmid; vector; transportation; degradation; metabolism; host range; nitrogen fixation; nodulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rhizobium species symbiotic plasmid pNGR234.
                                                                                                                      Broughton
                                                                                                                                                                                                             20-MAY-1997;
12-JUL-1996;
                                                                                                                                                                                                                                                                  10-JUL-1997;
                                                                                                                                                                                                                                                                                                       22-JAN-1998.
                                                                                                                                                                                                                                                                                                                                            WO9802560-A2
                                                                                                                                                                                                                                                                                                                                                                             Rhizobium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV30459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAV30459 standard; DNA; 536165
                                                                                                                                                                                                                                                                                                                                                                                                               legume; plant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
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                                                                                                                                                       INST MOLECULAR BIOTECHNOLOGY.

LAB BIOLOGIE MOLECULAIRE PLAN
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                                                                                                                                                     BIOLOGIE MOLECULAIRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                Freiberg CB,
                                                                                                                                                                                                           97GB-0010395.
96EP-0730001.
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/product= "processing protease-like protein"
/note= "homologous to the PP gene"
466590..467021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /standard_name= "ORF L12"
/product= "protein similar to
of nitrogenase"
/note= "homologous to the NifH
461228..461545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  464736..466079
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product= "peptidase-like"

note= "homologous to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /standard_name= "ORF L13"

(product= "protein of unknown function')

432201..464739
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/product= "protein of unknown f
/note= "homologous to the Nifx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard_name= "ORF L11"

product= "protein of unknown
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94.1%;
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                                                                                                                Perret XP,
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Pred. No. 4.3e+02;
0; Mismatches 1;
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                                                                                                                                                   PLANTES SUPERIE.
                                                                                                                Rosenthal
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bl-MPP gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NifH
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                   nitroger
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                                    used to
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Claim 1;

Fig

3; 228pp;

the nucleotide

**equence** English

of the plasmid pNGR234a isolated from

Rhizoblum sp. NGR234. Open reading frames (ORF) derivable from the nucleotide sequences or ORFs can be used e.g. in the transportation of compounds to and from an organism which is a host to at least one of the nucleotide sequences, ORFs or proteins, the degradation and/or metabolism of organic, inorganic, natural or xenobiotic substances in a host organism or the modification of the host range, nitrogen fixation abilities; for obtaining a synthetic minimal set of ORFs required for functional Rhizoblum-legume symbiosis,

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M. capsulatus, and for studying gene expression on a genomic scale and in gene expression assays of M. capsulatus genes. The sequences shown in ABQ90016-ABQ91855 represent M. capsulatus genes for use in arrays of the invention.
                                                                    The invention relates to a novel DNA array giving a representation of number of Methylococcus capsulatus genes. The method of the invention useful for determination of the differential expression of the genes c
                                                                                                                                                        Novel DNA array useful for determining differential expression of Methylococcus capsulatus genes, comprises polynucleotides or oligonucleotides representative for a selective number of Methylococcus
                                                                                                                       Claim 14; Page
                                                                                                                                                                                                                                             Birkeland NK,
Lillehaug JR,
                                                                                                                                                                                                                                                                                                                                                            14-JAN-2002; 2002WO-NO00019
                                                                                                                                                                                                                                                                                                                                                                                                                                     Methylococcus capsulatus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Micro array; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M. capsulatus
                                                                                                                                               capsulatus
                                                                                                                                                                                                           WPI; 2002-557818/59
                                                                                                                                                                                                                                                                                                                                                                                      18-JUL-2002
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                                                                                                                                                                                                                                                                                    (UNIF-) UNIFOB (TIGR-) TIGR.
                                                                                                                                                                                                                                                                                                                        12-JAN-2001;
12-JAN-2001;
                                                                                                                                             genes
                                                                                                                                                                                                                                                                                                                        2001NO-0000235.
2001NO-0000239.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
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                                                                                                                                                                                                                                             Eidhammer I,
Lossius I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #1578 for DNA array.
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                                                                                                                      678pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          differential expression; gene expression.
                                                                                                                                                                                                                                               Eisen JA,
                                                                                                                                                                                                                                                         Jonassen
                                                                                                                                                                                                                                               Fraser
                                                                                                                                                                                                                                             Jensen HB, Lien T
ser CM, Durkin AS;
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Sequence 144

BP; 30

P ;

50

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Η.

0 other;

RESULT 14
ABQ65658/c
ID ABQ6566
XX
AC ABQ6566

ABQ65658

standard; DNA; 705

BP.

0

ABQ65658

18

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RESULT 13
AB091594/c
ID AB0915
XX AB0915
XX Micro
DT 01-OCT
XX Micro
OS Methy]
XX Wicro
OS Methy]
XX I2-JA
PR 12-JA
PR (TIGR
XX UNIT Caps:
XX Nove:
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Best Local S
Matches 17
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Best Local S
Matches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                              M. capsulatus, and for studying gene expression on a genomic scale gene expression assays of M. capsulatus genes. The sequences shown ABQ90016-ABQ91855 represent M. capsulatus genes for use in arrays of the capsulatus genes genes for use in arrays of the capsulatus genes gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel DNA array useful for determining differential expression of Methylococcus capsulatus genes, comprises polynucleotides or oligonucleotides representative for a selective number of Methylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABQ91594 standard; DNA; 309 BP
                                                                                                                                                                                                                                                                                                                      Sequence 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a novel DNA array giving a representation of number of Methylococcus capsulatus genes. The method of the invention useful for determination of the differential expression of the genes of the differential expression of the genes of the genes of the differential expression of the genesic expression of the ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Birkeland NK,
Lillehaug JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Birkeland
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12-JAN-2001; 2001NO-0000239
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125
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                                                                                                                                                         l Similarity
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    CTGATCGCCATACGGCGAC 106
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                                                                            CTGATCGCCAAACGAGCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page
                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                      B₽;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       604; 678pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eidhammer I, Jonassen
Lossius I, Eisen JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STIFTELSEN UNIV BERGEN
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                                                                                                                                                                                                                                                                                                                      A; 86 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76.0%;
85.0%;
                                                                                                                                                                                           76.0%;
85.0%;
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Pred. No. 2.9e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                         0,
                                                                                                                                                                                                   Score 15.2;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                      109 G;
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                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                           63
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Fraser
                                                                                                                                                                                                                                                                                                                           Ţ,
                                                                                                                                                                                                   .1e+02;
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                                                                                                                                                                                                                                              DB
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ser CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           멂
                                                                                                                                                                                                                                                                                                                           0 other;
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Durkin
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                                                                                                                                                                                                                                              309;
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433213

TGATCGCCAATCGAGCA 433197 TGATCGCCAAACGAGCA

18

ABQ91593;

ABQ91593 standard;

DNA;

144

ВР

Query Match Best Local S Matches 16

Similarity

77.0%; 94.1%;

16;

Conservative

0

Score 15.4; D Pred. No. 4.3e 0; Mismatches

.3e+02

DB 19;

Length Indels

Gaps

0

Sequence 536165 BP; 111291 A; 155755 C;

157864 G;

111255 T; 0 other; 536165; 0,

especially for nodulation efficiency on host plants.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis
                                         Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-JAN-2001; 2001US-0770149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-JAN-2000; 2000US-178506P
                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MATH/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PRIC/
                                                                                                                                                                                                                                                                                                                                                   Gorlach
Rameaka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (WOES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAMI/)
                                                                                                                                                                                                                                                           New nucleic acid that hybridizes to Arabidopsis thaliana sequences, useful e.g. for preparing transgenic plants with increased resistano or altered metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                  (DAVI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RAME/
                                                                                                                           The invention relates to nucleic acids (I) that hybridise under stringent conditions to any of 999 sequences (ABQ65424-ABQ66422) or their fragments. (I) are used to express the corresponding polypeptides (II) or produce genetically modified plant cells or transgenic plants, which to produce genetically modified plant cells or transgenic plants, which may have improved resistance to disease or stress, or altered may have improved resistance to disease or stress, or altered, nutritional or medicinal products), or generally any trait of interest, nutritional or medicinal products), or generally any trait of interest, or can be used to screen for biologically active agents (e.g. fungicides, or insecticides and antibiotics).
                                                                                                                                                                                                                                                                                                                            Hurban P;
                                                                                                                                                                                                                                                                                                                                        Garcia CA,
                                                                                                                                                                                                                                                                                                                                                                                  (HURB/)
                                                                                                                                                                                                                                                                                                                                                                                                                                         KRIC/
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GARC/
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HAAS/)
                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 235; 40pp + Sequence Listing; English.
                                                                                            Note: The sequence data for this patent did not form part of the specification, but was obtained in electronic format directly fro USPTO at segdata.uspto.gov/sequence.html?DocID=999909770149.
                                                                         Sequence
                                                                                                                                                                                                                                                                                                         2002-479224/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RAMEAKA J G.
PAGE A.
MATHEW A V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HAMILTON C M. PRICE J L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GORLACH J.
                                                                                                                                                                                                                                                                                                                                                                                                KRICKER M.
SLATER T.
DAVIS K R.
ALLEN K.
HOFFMAN N.
                                                                                                                                                                                                                                                                                                                                                   Įģ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAAS W D.
GARCIA C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RAINES T M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WOESSNER J
                                                                                                                                                                                                                                                                                                                                                                                    HURBAN P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEDFORD B L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             thaliana
                                             Similarity
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                                                                                                                                                                                                                                                                                                                                         An Y, Hami
, Page A, M
, Kricker M,
CTGATCGCCAAACGAGCAAC
                                                                              705 BP; 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polynucleotide
                                                                                                                                                                                                                                                                                                                                                                  Hamilton CM,
                                                                                                                                                                                                                                                                                                                                              Mathew AV,
M, Slater T,
                                                                               A; 135
                                                76.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e cress; plant; transgenic; GMO; disease; biosynthetic pathway; nutrition; fungicide;
                                                                                C; 183 G;
                                        0;
                                                  score 15.2;
pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                   Price JL, Ra
Ledford BL,
f, Davis KR,
                    20
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                                         Mismatches
                                                                                     200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NO 235
                                                      .4e+02
                                                                 В
                                                                                    T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                        Raines TM,
                                                                                                                                                                                                                                                                                                                                                    Woessner
Allen K,
                                                                 24;
                                              Indels
                                                                 Length
                                                                                                                                                                                                                                                                                                                                                         Yu Y;
JP, Haas WD;
Hoffman N;
                                                                      705;
                                                                                                                                                                                                                                                                                        resistance
                                                  0
                                                Gaps
                                                     0
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Query Match

1281 BP;

300 A; 358

C; 333 Score

76.0%;

15.2;

B 25;

Length 1281;

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RESULT 15
ABT18455
ID ABT18
XX
AC ABT18
XX
The invention relates to novel purified or isolated nucleic acids of cessential genes of Aspergillus fundgatus. The isolated nucleic acids of the invention are used to treat or prevent infectious by a pathogenic companism such as A. fundgatus, to treat a non-infectious disease in a companism such as A. fundgatus, to treat a non-infectious disease in a pathogenic companism such as A. fundgatus. The polynucleotides are useful for companism funding the pathogenic companism of an object companism invade or reside, for companing with the pathogenic expressing recombinant protein for characterisation, screening or companisms invade or reside, for companing with the pathogenic companisms to identify duplicated genes or paralogues having the same or companism to identify duplicated genes or paralogues having the same or companism to identify and/or function, for companisms to identify similar biochemical activity and/or function, for companism to identify sequences of other related or distant pathogenic organisms to identify and sequences of other related or distant pathogenic organisms to identify and corporate or to interest to a pathogenic organism to identify and response, for salecting and corporate or to interest or to identify into the pathogenic organism to the protein antibodies, as an organism or companism to the pathogenic organism in another immune response, and for identifying polynuclectides encoding the other protein corporate in munice and for identifying polynuclectides encoding the other protein corporate in munice polynephides may be used to raise antibodies or to elicit immune response, as a reagent in assays designed to quantitatively isolate correlative receptors or ligands in the case or virulence corporate in which pathogenic organism invade or reside, and to companism invade or reside, and to companism to interest or interest or interest or organism invade or reside, and to companism to the interest or interest 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-APR-2001; 2001US-285697P.
27-APR-2001; 2001US-287066P.
05-UUN-2001; 2001US-25890P.
09-UUL-2001; 2001US-303899P.
31-AUG-2001; 2001US-316362P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABT18455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABT18455 standard; DNA; 1281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fungicide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aspergillus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-093124/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jiang B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ELIT-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aspergillus fumigatus, useful
A. fumigatus, or for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New purified or isolated nucleic acids of essential genes of Aspergillus fumigatus, useful for treating or preventing infections A. fumigatus, or for treating a non-infectious disease in a subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      de; cytostatic; essential gene; Aspergillus fumigatus; infection; contamination; biofilm; antibody; immune response; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTCATCGCCAGACGAGCACC 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tishkoff D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fumigatus essential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Run
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database
          O
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             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq length: 0 seq length: 2000000000
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1: /cgn2 6/ptodata/2

2: /cgn2 6/ptodata/2

3: /cgn2 6/ptodata/2

4: /cgn2 6/ptodata/2

5: /cgn2 6/ptodata/2

6: /cgn2 6/ptodata/2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        569978 seqs, 220691566 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                                                          74.0
74.0
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/cgn2_6/ptcdata/2/ina/5B_COMB.seq:*
/cgn2_6/ptcdata/2/ina/6A_COMB.seq:*
/cgn2_6/ptcdata/2/ina/6B_COMB.seq:*
/cgn2_6/ptcdata/2/ina/BCTUS_COMB.seq:*
/cgn2_6/ptcdata/2/ina/backfles1.seq:*
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3032
536165
36470
1664976
                             GenCore version 5.1.6 (c) 1993 - 2004 Compugen
  4 US-09-328-35-643
4 US-09-221-017B-347
4 US-09-214-808-1
4 US-08-311-731A-123
4 US-08-916-421B-1
1 US-07-912-900-25
1 US-08-285-309-25
2 US-08-285-309-25
2 US-08-107-532A-2028
1 US-09-107-532A-2028
1 US-09-107-532A-2028
1 US-09-103-840A-1
3 US-09-103-840A-1
3 US-09-103-840A-2
3 US-09-103-840A-2
3 US-09-103-840A-1
4 US-09-480-884A-1
4 US-09-480-884A-218
4 US-09-480-884A-60
1 US-09-480-984-60
1 US-09-480-984-60
1 US-09-480-984-60
1 US-09-542-615A-60
1 US-09-542-615A-60
1 US-09-66-421B-60
1 US-09-66-751-108
US-09-66-751-108
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Sequence 643, App sequence 147, App sequence 1, Appli sequence 1, Appli sequence 1, Appli sequence 25, Appl sequence 25, Appl sequence 31, Appl sequence 31, Appl sequence 17, Appl sequence 17, Appl sequence 17, Appl sequence 18, Appl sequence 218, Appl sequence 60, Appl sequenc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 643
LENGTH: 1698
TYPE: DNA
ORGANISM: Acinetobacter baumannii
US-09-328-352-643
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US-09-328-352-643/c
; Sequence 643, Application
; Patent No. 6562958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
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FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04

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Length 1698;

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US-08-996-685-7	99	-08-989-478-7	-08-	-80	US-08-989-478-11	-08-996-685-9	US-08-989-478-9	US-09-107-532A-858	US-09-328-352-1571	-08-996-685-13	3-08-989-478-13	-60	US-09-221-017B-199	US-09-232-149A-36	US-09-352-616A-36	-09-439-313-36	** *** *** ***
996	996	989	989	996	989	996	989	107	328	996	989	252	221	232	352	439	
-68	-996-685-6	-47	-989-478-6	-996-685-11	-47	-68	-47	-53	-35	-68	-47	-99	-01	-14	-61	-31	
5-7	5-6	8-7	9-6	5-1	8-1	5-9	8-9	2A-	2-1	5-1	8-1	1A-	7B-	9A-	6A-	3-3	,
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## ALIGNMENTS

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RESULT 2
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                                                                                                                                                                                                                                                                                    Sequence 3'
Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 16; Conservat
         COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,017B
APPLICATION NUMBER: US/09/221,017B
                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                       APPLICANT: ROSS, Bru
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                           STREET: 755 PAGI
                                                                                                                                                  STATE:
                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                             143
                                                                                                                                                                                                                                                                                    347, Application US/09221017B
o. 6444799
                                                                                                                                                                                                                                                                                                                                                                                                          4 ATCGCCAAACGAGCAAC
                                                                                                                                                                                                                                                                                                                                                                            ATCGCCAAACCAGCAAC 127
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                                                                                                                                                                            E: MORRISON & FOERSTER
755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
23-DEC-1998
                                                                                                                                                                                                                                  Bruce C.
N: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
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94.1%;
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Pred. No. 44
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                                           2.0b
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APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:

PCT/AU98/01023

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FILING DATE: 30-JA

30-JAN-1998

PP2911

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP11
FILING DATE: 31-DEC-1997 PRIOR APPLICATION DATA:

PP1182

NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 3032 base pairs
TYPE: nucleic acid
STRANDEDNESS: double

347:

TELEFAX: TELEPHONE:

650-494-0792

650-813-5600

REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:

27340-20021.00

Monroy, Gladys H

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; SEQ ID NO 1
; LENGTH: 536165
; LENGTH: 536165
; TYPE: DNA
; ORGANISM: Rhizobium
US-09-214-808-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-214-808-1/c
                                                                                                                                                                                                                                                                                                                APPLICANT: Rosenthal, Andre
APPLICANT: Freiberg, Christoph
APPLICANT: Perret, Kavier Philippe
APPLICANT: Berughton, William John
TITLE OF INVENTION: Genomic Sequence of Rhizobium SP. NGR 234 Symbiotic
Patent No. 6475793
TITLE OF INVENTION: Plasmid
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09214808A Patent No. 6475793
                                                                                                                                                                                          PRIOR APPLICATION NUMBER: PCT/IB97/00950
PRIOR FILING DATE: 1997-07-10
NUMBER OF SEQ ID NOS: 1
                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/214,808/
CURRENT FILING DATE: 1999-06-22
                                                                                                                                                                                                                                                                                                FILE REFERENCE:
                                                                                                                                                                        SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION:
                                                                                                                                                                    PatentIn
                                                                                                                                                                                                                                                                                                   CARP0068
                                                                                                                                                                      Ver. 2.1
77.0%;
94.1%;
Score 15.4;
Pred. No. 80;
                 DB 4;
               Length 536165;
```

US-08-916-421B-1/c

sequence 1, Application US/08916421B Patent No. 6503729

GENERAL INFORMATION:
APPLICANT: Bult et al.
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococc
Patent No. 6503729
TITLE OF INVENTION: jannaschii

밁

2855 CTGATCGCCATACGAGC 2871

1 CTGATCGCCAAACGAGC 17

JS-09-221-017B-347

NAME/KEY: misc\_feature LOCATION: 1...3032

ANTI-SENSE: UNI ORIGINAL SOURCE: HYPOTHETICAL: MOLECULE TYPE:

UNKNOWN

circular

DNA (genomic)

ORGANISM:

PORYPHYROMONAS GINGIVALIS

Query Match

Local

h 77.0%; Similarity 94.1%;

Score 15.4; Pred. No. 4

DB 4;

Length 3032;

Conservative

<u>.</u>.

Mismatches

Indels

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RESULT 5
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                                                                                                                   Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 617/720-3500
TELEPAX: 617/720-2441
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 36470 base pairs
                                                                                                                                                                                                                                   MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
                                                                                                                                                                                                    ORIGINAL SOURCE: ORGANISM: MYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 411
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
STREET: 600 ATLANTIC AVENUE
CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: CO
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: MAO, JEN
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: SMITH, APPLICANT: MAO, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                  LENGTH: 36470 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: MASSACHUSETTS
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 433213 TGATCGCCAATCGAGCA 433197
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                                                 3894 CTAATCGCCACACAAGCAAC 3913
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                                                                              CTGATCGCCAAACGAGCAAC 20
                                                                                                                 Conservative
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                                                                                                                                                                                                    MYCOBACTERIUM LEPRAE
                                                                                                                                                                                                                                                                                    circular
                                                                                                                                                                                                                                                                     DNA (genomic)
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85.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US/08/311,731A
                                                                                                                                                                                                                                                                                                                                                                       123:
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                                                                                                                Score 15.2; D
Pred. No. 79;
0; Mismatches
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                                                                                                                                                 Length 36470;
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SOFTWARE: PatentIn version 3.1 SEQ ID NO 1 OTHER INFORMATION: n equals a, t NAME/KEY: misc\_feature LOCATION: (191989) . (191989) OTHER INFORMATION: n equals a, t NAME/KEY: misc\_feature LOCATION: (191995) . (191995) LOCATION: (234187) (234187)
OTHER INFORMATION: n equals a.
NAME/KEY: misc feature
LOCATION: (234220) (234220)
OTHER INFORMATION: n equals a.
NAME/KEY: misc feature CURRENT APPLICATION NUMBER: US/08/916,421B CURRENT FILING DATE: 1997-08-22 PRIOR APPLICATION NUMBER: US 60/024,428 PRIOR FILING DATE: 1996-08-22 NUMBER OF SEQ ID NOS: 3 TYPE: DNA
ORGANISM: Methanococcus jannaschii
FEATURE: OTHER INFORMATION: n equals NAME/KEY: misc feature LOCATION: (84773)..(84773) NAME/KEY: misc feature LOCATION: (148948)..(148948) OTHER INFORMATION: n equals NAME/KEY: misc\_feature LOCATION: (103998)..(103998) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (98266)..(98266) OTHER INFORMATION: n equals NAME/KEY: misc\_feature LOCATION: (98159)..(98159) OTHER INFORMATION: n equals NAME/KEY: misc feature LOCATION: (98120) . (98120) OTHER INFORMATION: n equals LOCATION: (234814)...(234814)
OTHER INFORMATION: n equals
NAME/KEY: misc\_feature NAME/KEY: misc\_feature LOCATION: (234187)..(2) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (231980)..(231980) OTHER INFORMATION: n equals a, OTHER INFORMATION: n equals a, OTHER INFORMATION: n equals OTHER INFORMATION: n equals NAME/KEY: misc\_fe LOCATION: (84812) OTHER INFORMATION: n equals OTHER OTHER INFORMATION: JAME/KEY: misc\_feature .OCATION: (163385)..(163385) ENGTH: INFORMATION: n equals a, INFORMATION: 1664976 misc feature (309398) .. (309398) feature feature reacure .. (98343) .. (84808) .. (84773) n equals n equals (84812) (98239) (28258) 9 Ð a, **B** a a, D) a, ŗ ŗ ū ŗ 'n ŗ ŗ ŗ Ĺ ŗ ŗ ŗ ŗ ŗ ŗ ŗ , Ĺ ņ ú ō ņ ņ ņ ú ú ú ú ņ 'n ó ú ú ú ņ 'n 8 õ ç õ õ မ္ or မ္ ဝူ or ö ç õ ç õ õ ဗူ 8 유 õ

LOCATION: (779455) ... (779455)
OTHER INFORMATION: n equals a, t
NAME/REY: misc feature
LOCATION: (779676) ... (779676)
OTHER INFORMATION: n equals a, t
NAME/REY: misc feature
LOCATION: (855539) ... (855539) NAME/KEY: misc feature LOCATION: (713652)..(713652) OTHER INFORMATION: n equals a, OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (1084830)..(1084830) OTHER INFORMATION: n equals a, NAME/KEY: misc feature NAME/KEY: misc\_feature LOCATION: (682442) . (682442) OTHER INFORMATION: n equals NAME/KEY: misc\_feature LOCATION: (312993)...(312993) OTHER\_INFORMATION: n equals NAME/KEY: misc feature LOCATION: (312837)..(312837) OTHER INFORMATION: n equals NAME/KEY: misc\_featur LOCATION: (1349473).. NAME/KEY: misc\_feature LOCATION: (1313224)..(1313224) NAME/KEY: misc\_feature LOCATION: (871619)..(871619) LOCATION: (741684)...(741684)
OTHER INFORMATION: n equals
NAME/KEY: misc\_feature NAME/KEY: misc\_feature LOCATION: (674435)...(674435) OTHER\_INFORMATION: n equals a, LOCATION: (657203) .(657203) OTHER INFORMATION: n equals LOCATION: (657081)..(657081)
OTHER INFORMATION: n equals
NAME/KEY: misc\_feature LOCATION: (622708) . (622708)
OTHER INFORMATION: n equals
NAME/KEY: misc\_feature NAME/KEY: misc LOCATION: (6005 LOCATION: (559167) . (559167) OTHER INFORMATION: n equals LOCATION: (319226)..(319226) OTHER INFORMATION: n equals OTHER INFORMATION: n equals LOCATION: (1310988)..(131098 OTHER INFORMATION: n equals OTHER INFORMATION: n equals LOCATION: (855539)..(855539)
OTHER INFORMATION: n equals a, LOCATION: (600992)..(600992) NAME/KEY: misc feature LOCATION: (559241)..(559241) OTHER INFORMATION: n equals a, NAME/KEY: misc\_ NAME/KEY: misc\_feature OTHER INFORMATION: n equals NAME/KEY: misc INFORMATION: n equals a, (1310988) . . (1310988) misc\_feature (1096846)..(1096846) (1130881) .. (1130881) feature feature reature feature feature (1349473) a, a ā ā a b D a DI CI a ' a, a ā Ø ŗ ŗ ŗ ŗ ŗ ŗ רָ Ļ 5 Ĺ ŗ Ç ŗ ŗ רָ ŗ ŗ ζ, ŗ ŗ Ĺ Ĺ Ĺ ŗ ŗ ç, ú ņ ū 'n ņ Ç 'n ņ ō ū ņ ņ ó ú ó ņ ū ņ ó ú ó ú ç မ္ပ õ or or õ õ o R 유 OĽ, 9 õ o R Or. õ or R or õ 9 õ õ or P ဝူ ö õ 9 ω ω ω ω Q g g ω ω ω g Q g ω 9 g ø 9 g ω ĽΩ ω ω ω

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Patent No. 5349125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/912,900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: n equals a, t, -08-916-421B-1
                             TELEFAX: (516) /42-1300
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: (1637998)...(1637998)
OTHER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                               STREET: 400
CITY: Garden City
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: (1664854)..(1664855)
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LOCATION: (1470091)..(1470091)
OTHER INFORMATION: n equals a,
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LOCATION: (1349491)..(1349491)
OTHER INFORMATION: n equals a,
                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: DIGIGIO, FRANK S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8633
FILECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
OCATION: (1603734)..(1603734)
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OCATION: (1569020)..(1569020)
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                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID TITLE OF INVENTION: PATHWAY ENZYMES AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1565938 CTTATAGCCAAACCAGCAAC 1565919
                                                         TELEPHONE: (516) 742-4366
TELEPHONE: (516) 742-4366
TELEPHONE: (516) 742-4366
                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                     FILING DATE:
              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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1 Similarity 85.0%;
17; Conservation
                                                                                                                                                                                                                                                                                                                              11530
: 543 base pairs
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400 Garden City Plaza
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lester, Diane R.
                                                                                         (516) 742-4343
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                                                                                                                                                                                                                                              Release #1.0, Version #1.25
                                                                                                                                                                                                               US/07/912,900
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Pred. No. 9
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; STRANDEDNESS;
; TOPOLOGY: line
; MOLECULE TYPE: I
US-08-285-309-25
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; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-912-900-25
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                                                          Query Match
Best Local Similarity
Matches 16; Conserv
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Patent No. 5
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' rocal Similarity
                                                                                                                                                                                                                     TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: DiGigiio, Frank S.
REGISTRATION UNMBER: 31,346
REFERENCE/DOCKET NUMBER: 8633
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 543 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: GENETIC SEQUENCES ENCODING A 3,5'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 03-AUG-CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Garden City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
69 TGATCGCCAAACTATCAA 86
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                          2 TGATCGCCAAACGAGCAA 19
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400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/08285309
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Cornish, Edwina C.
Kovacic, Filippa
Tanaka, Yoshikazu
Lester, Diane R.
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                                                          Conservative
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                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
                                                                                                                                DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                           03-AUG-1994
                                                                                                                                                              single
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88.9%;
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88.9%;
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                                                       Score 14.8; D
Pred. No. 80;
0; Mismatches
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Pred. No. 80;
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                                                                                    DB 1;
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                                                                                 Length 543;
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                                                        Indels
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RESULT 8 US-08-502-046-25 VS-08-502-046-25, Application US/08502046 Sequence 25, Application US/08502046 Patent No. 5861487

GENERAL INFORMATION:

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RESULT 9
US-08-313-075A-31
US-08-313-075A-31
Sequence 31, Application US/08313075A
Patent No. 5639870
Patent O. 5639870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/502,046
FILING DATE: 14-UUL-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (516) 742-434
TELEFAX: (516) 742-436
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/285
FILING DATE: 03-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Didiglio, Frank S.
REGISTRATION NUMBER: 31,34
REFERENCE/DOCKET NUMBER: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 543 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: 15
MOLECULE TYPE:
                                                                                                                                                                                                                      APPLICANT: Holton, Timothy A. APPLICANT: Cornish, Edwina C. APPLICANT: Tanaka, Yoshikazu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Tanaka, Yoshikazu
APPLICANT: Lester, Diane R.
TITLE OF INVENTION: GENETIC SEQUENCES ENCODING A 3,
TITLE OF INVENTION: HYDROXYLASE AND USES
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                   APPLICANT: Cornish, Edwina C.
APPLICANT: Tanaka, Yoshikazu
TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID
TITLE OF INVENTION: PATHWAY ENZYMES AND USES THEREFOR
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (516) 742-4343
OMPUTER READABLE FORM:
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STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
                     COUNTRY: U
                                                                          ADDRESSEE: Scully, Scott, Murphy & Presser STREET: 400 Garden City Plaza CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                ADDRESSEE:
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                                                         New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                    U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74.0%; Score 14.8; 88.9%; Pred. No. 8
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                                                                                                                                                                                                                                                                                                                                                   Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2028, Application US/09107532A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 230 901 SANS UR INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: UFILING DATE: 30-NOV-1CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
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FILING DATE: 25-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 07-JAN-1993
PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: ....STRANDEDNESS: 81...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE:
COMPUTER: IF
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LOCATION: 1..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 31,346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENGTH:
                                                                                                                                                       ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16;
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                                                                                                    COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
                                                                                                                                                                                                                            CITY: Waltham
STATE: Massachusetts
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
                                                                                                                                                                                                                 COUNTRY: USA
                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                  ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      547 base pairs
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                                                                                                                                                                                                                                                                 100 Beaver Street
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Pred. No. 80;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                and David Bush
AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEU
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NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...810
SEQUENCE DESCRIPTION: SEQ ID NO: 2028:
US-09-107-532A-2028
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                                                                                                                                                                          COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,214A
FILING DATE: 26-JAN-1996
CLASSIFICATION: 536
ATTORNEY/AGENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17,
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TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 2028:
                                                            TELEFAX: (619) 535-890
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 3
                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-1
                                              SEQUENCE CHARACTERISTICS:
                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Yanofsky, Martin F.
RITLE OF INVENTION: Cauliflower Floral Meristem Identify
RITLE OF INVENTION: Genes and Methods of Using Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: circular MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
STRANDEDNESS:
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                               ENGTH:
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5811536
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: California
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TYPE: nucleic acid
STRANDEDNESS: double
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nucleic acid
EDNESS: double
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4370 La Jolla Village Drive, Suite 700
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                                                                                   535-8949
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Pred. No. 84;
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Patent No. 6127123
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                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION UNMBER: US 08/592.
PILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION UNMBER: 9-UD
REFERENCE/DOCKET NUMBER: P-UD
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 2095..2098
OTHER INFORMATION: /note= "N = one or more
OTHER INFORMATION: nucleotides."
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                                                                                LOCATION: 2095..2098
OTHER INFORMATION: //
OTHER INFORMATION: ni
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Campbell
OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                              LENGTH: 4379 base pairs
TYPE: nucleic acid
                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                  NAME/KEY:
                                                                                                                                   NAME/KEY: unsure
                                                                                                                                                                    ropology:
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16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1370 La Jolla Village Drive, Suite 700
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1..4379
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                                                  misc_feature
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                                                                                                                                                                                                                                                                                      (619)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cauliflower Floral Meristem Identity
Genes and Methods of Using Same
                                                                                                                                                                                                                                                                                        535-9001
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thaliana AP1 gene"
   /note= "sequence = Arabidopsis
thaliana AP1 gene"
                                                                                     nucleotides
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US-09-103-840A-1
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; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
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Matches
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Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                           SEQ ID NO 1
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                                  Matches
                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 2
                                                                                                    LENGTH: 4411529
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09103840A
Patent No. 6294328
                                                                                                                                                                                                        APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 198-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION UMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: FLEISCHMAN, Robert D. APPLICANT: WHITE, Owen R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.1
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TYPE: DNA
                             y Match 74.0%;
Local Similarity 88.9%;
les 16; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 88.1
168 16; Conservative
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3 GATCGCCAAACGAGCAAC 20
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88.9%;
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88.9%;
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                                Score 14.8; I
Pred. No. 89;
0; Mismatches
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; SOFTWARE: FastSEQ for Wi
SEQ ID NO 218
; LENGTH: 405
; TYPE: DNA
; ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
                                                                                                                                                                                                                                                      APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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APPLICANT:
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                                                       y Match 71.0%;
Local Similarity 84.2%;
hes 16; Conservative
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                        1 CTGATCGCCAAACGAGCAA 19
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CTGATGTCCAAAAGAGCAA 95
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Fanger, Gary R.
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Search completed: February 12, 2004, 06:08:10 Job time: 48.3171 secs

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Result
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Perfect score:
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1: /cgn2_6/ptodata/1/pubpna/US07_
2: /cgn2_6/ptodata/1/pubpna/US05_
3: /cgn2_6/ptodata/1/pubpna/US05_
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/Cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
/Cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
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/Cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
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12 US-09-770-149-235

15 US-10-128-714-2119

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US-09-878-574-7065
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Sequence 15, Appl
Sequence 7065, Ap
Sequence 4681, Ap
Sequence 240, App
Sequence 240, App
Sequence 2, Appli
Sequence 2, Appli
Sequence 211, Ap
Sequence 221, Ap
Sequence 2021, Ap
Sequence 2021, Ap
Sequence 2021, Ap
Sequence 2064, Ap
Sequence 26644, Ap
Sequence 116, App
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US-10-138-701-60 US-10-398-221-1962	9	US-10-027-632-173804	US-10-027-632-173804	US-10-029-386-684	US-09-864-408A-3499	US-10-156-761-1	US-10-128-714-5380	US-10-128-714-380	0	US-09-938-842A-1537	US-09-938-842A-1537	US-10-369-493-45576	US-10-108-260A-936	US-10-369-493-36531	US-10-142-835-29	US-10-156-761-350	US-10-036-959B-2	US-10-369-493-31049	US-10-369-493-28292	US-09-983-965-623	US-09-983-965-958	US-09-960-352-5967	US-10-369-493-33107	US-10-369-493-32914	US-10-079-854-216	US-09-764-878-216	US-10-128-714-219	US-10-108-605-324
Sequence 60, Appl Sequence 1962, Ap	ω				Sequence 3499, Ap	Sequence 1, Appli		Sequence 380, App				Sequence 45576, A	936,	365		35	Sequence 2, Appli	31	28292		958,	Sequence 5967, Ap	331		e 216	Sequence 216, App	219	Sequence 324, App

## ALIGNMENTS

US-10-001-073-15 RESULT 1

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RESULT 2
US-10-369-493-44911/c
US-10-369-493-44911/c
Sequence 44911, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
. APPLICANT: Chen, Xianfeng
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15, Application US/10001073

Publication No. US20030113725A1

GENERAL INFORMATION:
APPLICANT: Liggett, Stephen
APPLICANT: Small, Kirsten
ITILE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
ITILE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
ITILE REFERENCE: 13073-PCT
CURRENT APPLICATION NUMBER: US/10/001,073

CURRENT FILING DATE: 2001-11-01

NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 15
LENGTH: 20
TYPE: DNA
ORGANISM: Homo sapiens
US-10-001-073-15
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100.0%; Pred. No. 0.57;
Pative 0; Mismatches
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SEQ ID NO 7065
LENGTH: 277
TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: 701099380H1
US-09-878-574-7065
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; ORGANISM: Xenorhabdus nematophilus
US-10-369-493-44911
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US-09-878-574-7065/c
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SEQ ID NO 44911
LENGTH: 3325
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR APPLICATION DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
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                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Byrum, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4681, Application US/09878574 Patent No. US20020110548A1
SEQ ID NO 4681
                       APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael J.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
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Local Similarity 89.5%;
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; LOCATION: (1)..(1976)
; OTHER INFORMATION: unBure at all n locations
; OTHER INFORMATION: Clone ID: LIB3028-039-Q1-B2-G12
US-09-878-574-4681
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                                                                                                                    ; ORGANISM: Homo sapiens US-10-079-854-240
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LENGTH: 5786
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                                                                                                                                                             SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 240
LENGTH: 5786
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Publication No. US20
GENERAL INFORMATION
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                                                         Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA121
CURRENT APPLICATION NUMBER: US/09/764,878
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prior application data removed - consult PALM NUMBER OF SEQ ID NOS: 428 SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                           Prior Application removed - NUMBER OF SEQ ID NOS: 428
                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/079,854
CURRENT FILING DATE: 2002-02-22
                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Nucleic Acids, Proteins, FILE REFERENCE: PA121C1
                                                                                                                                                                                                                                                                                                      APPLICANT: Rosen et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Glycine max
FEATURE:
                                                                                                                                                    TYPE: DNA
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TTATCGCCAAATGAGCAAC 836
                              TGATCGCCAAACGAGCAAC 20
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o. US20030054368A1
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85.0%;
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89.5%;
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Pred. No. 1.8e
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Pred. No. 1.6e+02;
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                                                                          Score 15.8;
Pred. No. 1
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PRIOR APPLICATION NUMBER: 2001-01-26
PRIOR FILING DATE: 2001-01-26
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTMARE: FastSEQ for Windows Version 4
SEQ ID NO 235
LENGTH: 705
TYPE: DNA
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US-09-770-149-235/c
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Publication No. US20030054522A1
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                                                                                                                                                                             APPLICANT: Hoffman, Neil
APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: thaliana
FILE REFERENCE: 2024 (PARA-013PRV)
CURRENT APPLICATION NUMBER: US/09/770,149
CURRENT FILING DATE: 2001-01-26
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APPLICANT: Freiberg, Christoph
APPLICANT: Perret, Xavier Philippe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/939,964
CURRENT FILING DATE: 2001-08-27
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TYPE: DNA
ORGANISM: Rhizobium
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                                      ORGANISM: Arabidopsis thalians
AME/KEY: misc_feature
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Local Similarity 94.1%;
es 16; Conservarion
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                                                                                                                FastSEQ for Windows Version 4.0
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Allen, Keith
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                                                                                                                                                                                                                                                                                                                                                                                                          Woessner, Jeffrey P. Haas, William David
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Ledford, Brooke L.
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Hamilton, Carol
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Pred. No. 4.
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; PUDILICALLY.....;
GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Wengi
; APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Tishkoff, Daniel
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; OTHER INFORMATION: n = A,T,C or G
US-09-770-149-235
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US-10-128-714-2219
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CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-07-09
PRIOR FILING DATE: 2001-07-09
PRIOR FILING DATE: 2001-07-09
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               APPLICANT: Zamudio, Carlos
APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-999
CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WHICH FILING DATE: 2001-08-31 NUMBER OF SEQ ID NOS: 8603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
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APPLICATION NUMBER: US 60/285,697
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Zamudio, Carlos
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85.0%;
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Pred. No. 3.
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Pred. No. 3
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                                                                                                      in Aspergillus fumigatus
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US-09-938-842A-2021/c
Sequence 2017, Application US/09938842A
Publication No. US20040009476A9
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Aspergillus fumigatus US-10-128-714-2219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-07-09
PRIOR FILING DATE: 2001-08-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2021, Application US/09938842A Patent No. US20020160378A1 GENERAL INFORMATION:
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SEQ ID NO 2021
LENGTH: 1359
                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local Similarity
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LENGTH: 1284
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APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Kreps, Jeef
APPLICANT: Kreps, Jeel
APPLICANT: Kreps, Jeel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Arabidopsis thaliana
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1 Similarity 85.0%;
17; Conservation
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Pred. No. 3.3e+02;
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Pred. No. 3.
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; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; PRIOR FILING DATE: 2001-06-22
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 206
LENGTH- 2031
TYPE: DNA
ORGANISM: Drosophila melanogaster
                                                                                                                                                                Sequence 6644, Application US/09815242 Patent No. US20020061569A1
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SEQ ID NO 2021
LENGTH: 1359
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Best Local Similarity
Matches 17; Conserv
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Publication No.
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PRIOR APPLICATION NUMBER: US 60/176,418
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 31133B
CURRENT APPLICATION NUMBER: US/10/108,605
CURRENT FILING DATE: 2002-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bachmann, Jane
APPLICANT: Kamdar, Kim
APPLICANT: Kamdar, Kim
TITLE OF INVENTION: NUCLBIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE
TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 09/761,142
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APPLICANT: Stam, Lynn
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Bachmann, Jane
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o. US20020160934A1
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85.0%;
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85.0%; Pred. No. 3.3e+02;
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Pred. No. 3.
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APPLICANT: Stam, Lynn
APPLICANT: Kamdar, Kim
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE
TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
FILE REFERENCE: 31133B
CURRENT APPLICATION NUMBER: US/10/108,605
CURRENT APPLICATION NUMBER: US/00-03-27
PRIOR APPLICATION NUMBER: US/09/761,142
PRIOR APPLICATION NUMBER:
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR PRIOR PRIOR DATE: 2000-12-22
PRIOR PRIOR PRIOR DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PRIOR PRIOR DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOPTWARE: FABSUSEQ for Windows Version 4.0
SEQ ID NO 6644
LENGTH: 203
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ORGANISM: Enterococcus faecalis
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(2193)
US-09-815-242-6644
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US-10-108-605-116
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Best Local Similarity
Matches 17; Conserv
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Best Local Similarity
Matches 17; Conserv
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783 CCGATCGCCAACGCCCAAC 802
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                                               CTGATCGCCANACGAGCAAC 20
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85.0%;
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Pred. No. 3.5e+02;
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BE033222 133577 MA
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DEFINITION
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                                                                                                                                                                                                                                             Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 275)
Stapleton, M., Brokatein, P., Hong, L., Tyler, D., Berman, B., Carlson, J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Misra, S., Mungall, C.J., Nunco, J., Pacleb, J., Paragas, V., Park, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Celniker, S. and Rubin, G.M.
                                                                                                                                                           B1372571 275 bp mRNA linear E
RE59566.5prime RE Drosophila melanogaster normalized
Drosophila melanogaster cDNA clone RE59566 5, mRNA se
B1372571
 Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA
Fax: 510 486 6798
                             Unpublished
Contact: Sta
                                             BDGP/HHMI RE Drosophila
                                                                                                                                                   BI372571.1 GI:15068599
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N8291
B1946431
B1946431
B1946431
BH962262
BH67437924
BH5693943
AGG771544
BH2694943
AGG71544
BF45127
BF451273
BF451274
BF45126663
BH365931
BH776626
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         USA
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BI946222 odg10b08.
BH674374 BOMNIJ3TF
BH56236 BOGYL18TF
BH56336 BOGYL18TF
BH569343 BOHVAR9TF
AG071.544 Pan trog1T
CD255409 AGENCOURT
BG253789 60236671
AL273862 Tetracdon
BX293513 Arabidops
AC083928 Arabidops
AC083928 Arabidops
BX293513 Arabidops
C65542 C65542 Yuji
BJ28930 BJ284930
BF451274 Uz68all 0.
BF451274 BJ28670630
BF451274 BJ28670630
BF451274 BJ28670630
BF457549 UT-M-B21-BU386746 603860053
BJ73374 Sai99h01
AJ39627 BST271509
BF457549 UT-M-B71-BU386766 003860053
BJ73374 Sai99h01
AJ197627 EST271509
BM328798 BF1C1 26 F
BQ7770626 UT-M-F70-BM328798 BTC1 26 F
BQ7770626 UT-M-F70-BH329921 MGX-408003M
BJ122635 BJ122635
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sequence.

George

EST 01-AUG-2001 Embryo pflc-1

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plate: RE.595 row: F column: 6
High quality sequence stop: 246.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Epermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 428)

Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18;
                                                                                                                                                                                                                                                                                                                                               Contact: Joseph R. Ecker Salk Institute Genomic Analysis Laboratory The Salk Institute for Biological Studies 11010 N. Torrey Pines Road, La Jolla, CA 92 Tel: 858 453 4100 x1752 Fax: 858 558 6379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BH756337 428 bp DNA linear GSS SALK 053523.55.75.x Arabidopsis thaliana TDNA insertion Arabidopsis thaliana genomic clone SALK 053523.55.75.x,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     survey sequence.
BH756337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis Genome 
Unpublished
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                                                                                                                                                                                                                                                              TDNA tagged
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/dev_stage="0-24 hours mixed stage embryonic"
/lab_host="DH5-alpha TonA"
/clone_lib="RE Drosophila melanogaster normalized
pFlc-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: embryo; Vector: pFlc1; Site_1: XhoI; Site_2: BamHI; Library was kindly generated by Piero Carninci at the RIKEN. The library was normalized and excised using Cre recombinase. Plasmid cDNA library."

74 C 67 g 57 t
/db_xref="taxon:3702"
/clone="SALK 053523.55.75.x"
/clone=lib="Arabidopsis thaliana TDNA insertion lines"
/clone=lib="Arabidopsis thaliana TDNA insertion lines
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
                                                                                                                                                       /strain="Columbia 0"
                                                                                                                                                                            mol_type="genomic
                                                                                                                                                                                                organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                       Socation/Qualifiers
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94.7%;
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L.3e+02;
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303
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Plate: 68 row: L column: 5
Seq primer: ATTTAGGTGACACTATAG
Location/Qualifiers
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Mammalia; Eutheria;
1 (bases 1 to 561)
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                                                      l Similarity
18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fahrenkrug,S.C., Smith,T.P.L., Freking,B.A., Cho,J.,
Vallet,J., Wise,T., Rohrer,G.A., Pertea,G., Sultana,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sus scrofa (pig)
                                                                                                                                                                                                                                                                                                                                                                                           Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 402 762 4366
Fax: 402 762 4390
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CTGATCGACAGACGAGCAAC
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nilarity 90.0%;
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                                                                                                                   /clome lib="MARC 1PIG"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from day 11, 13, 15, 20
and 30 embryos."
a 179 c 135 g 117 t
                                                                                                                                                                                                   /tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9823"
                                                                                                                                                                                                                                                             organism="Sus scrofa"
                                                                                                                                                                                                                                                                               .561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                site of insertion. Details of the protocols used can ound at http://signal.salk.edu/tdna_protocols.html" 86 c 101 g 146 t
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90.0%;
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Cetartiodactyla; Suina; Suidae;
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Pred. No. 3
                                                                       Score 16.8;
Pred. No. 3
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Sus.
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RESULT 4 BG636450

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BG381314 GI:13305786 EST.
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               μ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        300 BG636450 700 SD14169.Sprime SD Drosophila pOT2 Drosophila melanogaster CG17509: FBan0017509 located
                                                                                      Bonaldo, M.F., Lennon, G. and Some Normalization and subtraction:
                                                                                                  1 (bases 1 to 359)
Bonaldo, M.F., Lenno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003823: arm:2R [6997351,7260081]
estimated-cyto:48D8-48F5: 04/13/2001
Plate: SD.141 row: F column: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Harvey, D., Brokstein, P., Hong, L., Lewis, S. and Rubin, G.M.
                                                    Genome Res. 6 (9),
                                                                     discovery
                                                                                                                                            Rattus.
                                                                                                                                                                                                                      Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 636.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BDGP/HHMI Drosophila EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 700)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pOT2; Site 1: EcoRI; Site 2: Xho1; Sized fractionated cDNAs were directly ligated into pOT2. Plasmid cDNA library."
186 c 173 g 145 t
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/clone_lib="SD Drosophila melanogaster Schneider L2 cell
culture pOT2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="texon:7227"
/clone="SD14169"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84.0%;
90.0%;
                                                    791-806 (1996)
                                                                                                                                                        Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 16.8; DB 10;
Pred. No. 3.7e+02;
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                                                                                                        Soares, M.B.
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                                                                                      two
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                                                                                    approaches
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                                                                                      facilitate
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                                                                                                                                                                                                                                                                                                              cDNA clone
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TGESTZy53d12.r1 TGRH Tachyzoite cDNA Toxoplasma tgzy53d12.r1 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 319 335 8250
Fax: 319 335 9565
Email: herro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST.
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The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com)
The following repetitive elements were found in this cDNA sequence: 73-206, >RSIME1#SINE/B4(B5)
                                                        Contact: Marra M
WashU-Merck EST Project
Washington University Sch
4444 Forest Park Parkway,
                                                                                                                                                                                                                                Hehl, A., Manger, I., Marra, M., Sibley, L.D., Dietrich, N., Dubuque, T., Hillier, L., Kuc. Waterston, R.H. and Boothroyd, J. WashU-Merck-Stanford-NIH Toxoplasma EST pr
                                                                                                                                                                                                                                                                                                                                                                      Sarcocystidae; Toxoplasma.

1 (bases 1 to 477)
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Toxoplasma gondii
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                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N82961.1 GI:1258714
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314 286 1810
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//dev stage="ADULT"
//dev stage="ADULT"
//lab_host="Ul-R-CT0" (Pharmacia) with a modified
//clone_lib="Ul-R-CT0" (Pharmacia) with a modified
//note="Vector: pT73D-Pac (Pharmacia) with a modif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAG_SEQ=None
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/db_xref="taxon:10116"
/clone="UI-R-CT0-bui-g-04-0-UI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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|mol_type="mRNA"
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94.4%;
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Pred. No. 4.7e+02;
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71 g
                                                               School of Medicine vay, Box 8501, St.
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                                                               Louis, MO 63108
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BI946431
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Seq primer: T3
High quality sequence
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17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 594)

Kucharski, R. and Maleszka, R.

Evaluation of differential gene expression during behavioral development in the honeybee using microarrays and northern b Genome Biol. 3 (2), research0007.1-9 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bEST28.5' Honeybee brain
                                                                                                                                                                                                                                 Biology Pl., Camberra ACT 0200, Australia
Tel: +61 2 6125 0451
Fax: +61 2 6125 3784
                                                                                                                                                                                                                                                                                                                           Visual Sciences Group
Research School of Biological Sciences, Australian National
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Apis mellifera (honeybee)
Apis mellifera
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                                                                                                                                                                                                                                                                                                                                                                                     Other_ESTs: bEST28.3'
                                                                                                                                                                                                                                                                                                         University
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Location/Qualifiers
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//clone="tgzy53d12.r1"
//lab host="XL1-Blue MRF'"
//lab host="XL1-Blue MRF'"
//lone="lb="TgRH Tachyzoite cDNA"
//clone_lb="TgRH Tachyzoite Swere grown in human
Toxoplasma RH strain tachyzoites were grown in human
foreskin fibroblast cultures in vitro. The library was
constructed by K.L. Wan, Cambridge University. cDNAs were
synthesized from polyA RNAs by oligo d(T) priming and
directionally cloned into the EcoRI to XhoI sites of the
Lambda ZapII vector using the ZAP-cDNA synthesis kit
(Stratagene). WARNING: the library contains a small
gercentage of cDNAs derived from the human host cells."
04 a 107 c 146 g 109 t 11 others
                                                                                                                                                                                                                 maleszka@rsbs.anu.edu.au
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Toxoplasma
                    /tissue_type="central brain,
    deuterocerebrum"
                                                                                                                              organism="Apis mellifera"
/dev_stage="adult worker"
                                                                   /sex="female"
                                                                                   db_xref="taxon:7460"
                                                                                                                                                                        ocation/Qualifiers
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                                                                                                            type="mRNA"
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Pred. No. 5.2e+02;
M4 smatches 1;
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                                             mushroom bodies, central body
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RESULT 9 BH674374/c

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RESULT 8
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Contact: Richard K. Wilson
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Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R.,
W., Rabinowicz,P.D. and Wilson,R.K.
Whole genome shotgun reads from Brassica oleracea
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odg10b08.b1 B.oleracea002 Brassica
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Washington University School of Medicine
Email: submissions@watson.wustl.edu
Plate: odg10 row: b column: 08
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/mol_type="genomic DNA"
/db xref="taxon:3712"
/clone lib="B.oleracea002"
/clone lib="B.oleracea002"
/note="vector: pOTw13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea T01000DH3 buds provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center."
90 a 197 c 175 g 137 t 1 others
                                                                           Conservative
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/clone lib="Honeybee brain cDNA library"
/note="Organ: brain; Vector: pBluescript II SK-; Site_1:
/note="Organ: brain; Vector: pBluescript II SK-; Site_1:
EcoRI; Site_2: XhoI; cDNA-harboring phagemids were
obtained by performing mass excission procedure on honeybee
brain cDNA lambda Unizap XR library (Ebert P.R. et al.,
1998, Insect Mol. Biol. 7(2):151-62)."

132 c 184 g 117 t
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              9712 Medical Center Drive, R
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdcown@tigr.org
DNA is from a doubled haploi
Seq primer: TF
                                                                                                                                                                         Brassica oleracea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid;
; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 765)

Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.

Whole genome shotgun sequencing of Brassica oleracea
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Brassica Coleracea
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
peurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 749)
Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.
Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.
                                                                                                                                     Whole genome shotgun sequencing Unpublished Other GSSs: BOGYI38TR Contact: Chris Town
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Fax: 301-838-0208
Email: cdcown@tigr.org
DNA is from a doubled haploid provided
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/note="Vector: pHOSI; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers" a 190 c 191 g 214 t
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/clone="BOMNJ43"
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/mol_type="genomic DNA"
/strain="TO100DH3"
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1 (bases 1 to 794)

Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M. Whole genome shotgun sequencing of Brassica oleracea
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Fax: 301-838-0208
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Unpublished
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DNA is from a doubled haploid
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                                                                                                                                                                  /clone_lib="BOGG"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb
genomic DNA inserted into pHOS1 using BstXI
genomic 221 c 170 g 162 t
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/mol_type="genomic DNA"
/strain="TO1000DH3"
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clone="BOGGE84"
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/strain="TO1000DH3"
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/clone="BOGYI38"
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Pred. No. 6.3e+02;
0; Mismatches 1;
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AG071544
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Matches 17
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1 (bases 1 to 806)

1 (bases 1 to 806)

1 (bases 1, Witherback, T., Koo, H. and Fraser, C.M.
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17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Chris Town
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:hhttp://hgp.gsc.riken.go.jp/, Tel:81-45-503-9170)
Tel:81-45-503-911, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end Clones are derived from the Chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                    Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
                                                                                                                                                                                                                                   Fujiyama,A., Hattori,M., Toyoda,A., Totoki,Y., Watanabe,H. and Sakaki,Y. BAC end sequences of Library PTB
                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                             AG071544
AG071544.1 GI:16623346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="BO_2_3 KB"
/rote="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared fonce="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers" a 167 c 239 g 232 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
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94.4%;
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Pred. No. 6.4e+C
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PTB-062M08.R,
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.6.4e+02;
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BOHVA49,
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                   Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892 Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST.
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CD255409.1 GI:31015875
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kenopodinae;
                                                                                                                                                                                                                                                             found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM14571 row: i column: 03
                                                                                                                                                                                                                                                                                                             cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GATCGCCAAACGAGCAAC 20
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R.Site 2
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                                                                                                                                                                                                                                         quality sequence stop:
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/clone_lib="PTB Chimpanzee Male BAC Library"
/s51 c 211 g 23 t 7 others
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/db_xref="taxon:9598"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'clone="PTB-062M08.R"
/clone="IMAGE:6951820"
/dev stage="adult"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/clone lib="WICHD XGC Brn1"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Technologies. Note: This is a Xenopus Gene Collection (XGC
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                                                                                                                                                                    organism="Xenopus laevis"
/mol_type="mRNA"
                                                                                                                                                  db_xref="taxon:8355"
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Pred. No. 6.6e+02;
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BG253789
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SOURCE
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Search completed: February 12, 2004, 06:05:58 Job time : 1087.71 secs
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM10299 row: n column: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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BG253789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 666.
Location/Qualifiers
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                                                                                                                                                                                                                                /tissue_type="adenocarcinoma, cell line"
/lab_host="NIH10B (phage-resistant)"
/clone_lib="NIH_MGC_91"
/note="Organ; prostate; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.4 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
a 226 c 208 g 200 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4474961"
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Maximum Match 100%
Listing first 45 summaries
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14: gb st:*

15: em fun:*

6: em fun:*

9: em mu:*

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

AUTHORS TITLE JOURNAL	ORGANISM	ACCESSION VERSION KEYWORDS	DEFINITION	RESULT 1 AX350504		0 C			C 40				ى رى د 4. 10		3 11 3				C (25)			c 20			c 16		. Д	c 11	بر د		) () B 7				2 P	Result No. S	
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to	Vertebrata; Euteleostomi; ; Hominidae; Homo.		Tinear PAT 06-FEB-2002			7254 Le	71336	67 0	51174 Felis cat	2526 Amb	427263 Dipus	w c	26994 Rat	16537 Dro	19 Dani	04510 Dro	116696 Mus	AC080148 Homo sapi AC083843 Homo sapi	17096 Homo sap	AC078903 Homo sapi AF159227 Homo sapi	34256 Sequence	2 Drosophi 0 Homo sab	315939 Tap	Dugong dug	323232 Arab	<u> </u>	J427259 Anomalu	7 Sue so	03 Homo sap	05900 Homo s	041 Human alp 48756 Semieno	70618 Sequenc	ສຸຄຸ	350490 Sequence	50504 Sequenc 742 Human alp	Description	

FEATURES

Liggett,

Stephen B. (US); Small, Kersten M. (US)

Location/Qualifiers

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Original source text: Human adult neuroblastoma DNA, clone PCRA2. Draft entry and computer-readable sequence for [Unpublished (1990)] kindly submitted by A.C.Chang, 20-SEP-1990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochem. Biophys. Res. Commun. 172 (2), 817-823 91054503
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Chang, A.C., Ho, T.F. and Chang, N.C.
In vitro amplification by polymerase chain reaction of
gene encoding the third subtype of alpha-2 adrenergic x
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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155, Sect II, Li-Noon St
Taipei, Taiwan, 11221 ROC
Location/Qualifiers
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/codon_start=1
/codon_start=1
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/proted:_id="AAA62823.1"
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EKEEGETPEDTGTRALPPSWAALPNSGQGXEGVGASPEDEAEREEEEEEEECEP
GAVPVSBASACSPPLQQPGGSKVLATLRGQVLLGRGVGAIGGQWWRRRAQLTREKRFT
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|_type="neuroblastoma"
| | type="neural"
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Alpha-2 adrenergic receptor polymorphisms
Patent: WO 0179561-A 2 25-OCT-2001;
Liggett, Stephen B. (US); Small, Kersten
Location/Qualifiers
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AX350490
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1 (bases 1 to 1344)

Small, K.M., Brown, K.M., Forbes, S.L. and Liggett, S.B.

Polymorphic deletion of three intracellular acidic residues of the alpha 2B-adrenergic receptor decreases G protein-coupled receptor kinase-mediated phosphorylation and desensitization J. Biol. Chem. 276 (7), 4917-4922 (2001)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                            2 (bases 1 to 1344)
Small,K.M., Brown,K.M., Forbes,S.L. and Liggett,S.B.
Direct Submission
Submitted (26-0CT-2000) Internal Medicine, Universit
Cincinnati, 231 Bethesda Ave, Cincinnati, OH 45267,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens alpha 2B
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
458 c 400 g 26
/organism="Homo sapiens"
/mol_type="genomic DNA"
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AX350489
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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ilarity 100.0%;
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APQNLELVSLAAADILVATLIIPSLANBLLGYWYFRRTWEEVYLALDVLFCTSSIVH
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RPQCKLNQBAWYILASSIGSFFAPCLIWILVYLRIYLLAKRSNRRGPRAKGGPGGES
KQPRPDHGGALASAKLPALASVASAREVNGHSKSTGEKEEGETPEDTGTRALPPSWAA
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
458 c 405 g 26
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TLRGQVLLGRGVGA1GGQWWRRRAQLTREKRFTFVLAVVIGVFVLCWFPFFFSYSLGA
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/db_xref="GI:12698670"
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RESULT 7
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Best Local
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                                                                                                                                                                                                                                                                                                                                   Original source text: Human placenta DNA, clone alpha-2 C2. Draft entry and computer-readable sequence for [1] kindly submitted by J.W.Lomasney, 03-MAX-1990, for release after publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Lomasney, J.W., Lorenz, W., Allen, L.F., King, K., Regan, J.W., Yang-Feng, T.L., Caron, M.G. and Lefkowitz, R.J. Expansion of the alpha 2-adrenergic receptor family: cloning and characterization of a human alpha 2-adrenergic receptor subtype, the gene for which is located on chromosome 2

Proc. Natl. Acad. Sci. U.S.A. 87 (13), 5094-5098 (1990)
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Au-Young, J. and Seilhamer, J. J.
Composition for the detection of signaling pathway gene expression
Patent: US 6500938-A 1181 31-DEC-2002;
Location/Qualifiers
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Sequence 1181 from patent
AR270618
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/db_xxef="GD8:G00-120-539"
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705 c 660 q
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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AF005900/c
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Sequence 41 from Patent W002061087.
AX548756
2 (bases 1 to 9842)
2 (bases 1 to 9842)
Cayla,C., Schaak,S., Bouloumie,A., Devedjian,J.C.
Direct Submission
Submitted (29-MAY-1997) INSERM Unit 317
CHU Rangueil. Toulous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Burmer, G.C., Roush, C.L. and Brown, J.P.
Antigenic peptides, such as for G protein-coupled receptors (GPCRs), antibodies thereto, and systems for identifying such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AX548756.1 GI:25813686
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Homo mapiens alpha2B-adrenergic
complete cds.
AF005900
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20; Conserv
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Patent: WO 02061087-A 41 08-AUG-2002;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Cayla,C., Schaak,S., Bouloumie,A.,
Alpha2C2-adrenergic receptor gene
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Mammalia; Eutheria; Primates;
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LPNSGQGOKEGVCGASPEDEAEEEEEEEEEEEEEECEPQAVPVSPASACSPPLQQPQGSR
VLATLRGQVLLGRGVGAIGGOWWRRAHVTREKRFTFVLAVVIGVFVLCWFPFFFSYS
LGAICPKHCKVPHGLFQFFFWIGYCNSSLNPVIYTIFNQDFRRAFRRILCRPWTQTAW
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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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100.0%; Pred. No. 10;
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AC092603 AC073396
AC092603.2 GI:16303539
           4 (bases 1 to 22842)
4 (bases 1 to 22842)
Waterston,R.H.
Direct Submission
Submitted (20-OCT-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                                        Martinka, S., Abbott, A., Hawkins, M., Elliott, G. and Doebber, A. The sequence of Homo sapiens BAC clone RP11-139J6 Unpublished (2001) 3 (bases 1 to 22842) Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 22842)
Sulston, J.E. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                 Direct Submission
Submitted (19-UUL-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
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/product="alpha2B-adrenergic receptor"
/product="alpha2B-adrenergic receptor"
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/protein_id="AbB62558.1"
/db_xref="GI:2245628"
/translation="MDHQDPYSVQATAAIAAAITFLILFTIFGNALVILAVLTSRSLR
/translation="MDHQDPYSVQATAAIAAAITFLILFTIFGNALVILAVLTSRSLR
ADQULFLVSLAAADILVATLLIIPFSLANELLGYMYFRRTWCEVYLALDVLFCTSSIVH
APQNLFLVSLAAADILVATLLIIPFSLANELLGYWYFRAVLIAVLSRSRRFBFLYGGDFQBFR
LCAISLDRYWAVSRALEYNSKRTPRRIKCIILTVNLIAKRSNRRGFRAKGGGPQGBFR
RPQCKLNQEAMYILASSIGSFFASACHTNLIVYLRIYLIAKRSNRFBDTGTRALPPSWAA
KPQCKLNQEAMYILASSIGSFFASACHTNLIVYLRIYLIAKRSACSPLOQDQGGSR
LLATLRGQVLLGRGVGAIGGQWWRRRAQLTREKRFTFVLAVVLGVFVLCWFPFFFSYS
VLATLRGQVLLGRGVGAIGGGOWRRRAQLTREKRFTFLNODFRRAFRRILCRFWTQTAW
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/gene="alpha2C2AR"
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/chromosome="2"
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RP11-139J6 from
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Submitted (01-MAR-2002) Department of Genetics, Washington Submitted (1994) Submitted (1994) Department of Genetics, Wissouri 63108, University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, On Oct 20, 2001 this sequence version replaced gi:14916188.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (23-OCT-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 (bases 1 to 22842) Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                          The clone sequenced to the left is RP11-401C13, 2000 bp overlap; the clone sequenced to the right is RP11-574017, 2000 bp overlap. Actual end of this clone is at base position 48999 of RP11-574017.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Waterston, R.H.
                                                                                                                                                                                                                                                                                                                The sequence of AC073396 has been Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NEIGHBORING SEQUENCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOURCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                     Polymorphisms have been identified between AC013272 and AC092603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------ Summary Statistics
Center project name: H_NH0139J06
Drafting Center: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://genome.wustl.edu/gscContact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Washington University Genome Sequencing Center Center code: WUGSC
                         /rpt_family="(TG)n"
1424. .1449
                                                                                                                 352.
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                                                                     /rpt_family="MIR"
1377. .1424
                                                                                                                                                                                                       /mol_type="genomic DN
/db_xref="taxon:9606"
/chromosome="2"
                                                                                                                                                                                map="2"
                                                                                                                                                                                                                                                                        'organism="Homo sapiens"
                                                                                                                                      clone_lib="RPCI-11"
                                                                                                                                                             clone="RP11-139J6"
    _family="(GA)n"
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/note="similar to
(NID:g12933576)"
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/note="similar to
(NID:g12886265)"
                                              15747
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14762. .14822
                                                                                                                 15110. .15648
                                                                                                                                    15084. .15487
/note="similar to Sus scrofa EST AW785035 (NID:g7841811)"
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12062. .12257
                                                                   (NID:g8082456) "
                                                                                          'note="similar to
                                                                                                                                                                           note="similar to"
(NID:g12877089)"
                                                                                                                                                                                                                                               note="CpG
                                                                                                                                                                                                                                                                                        note="similar to Homo (NID:g12877089)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="match to EST BF475329
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                                                                                          Rattus
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REFERENCE
AUTHORS
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VERSION
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aar2B gene; alpha adrenergic receptor 2B.
Phoca vitulina (harbor seal)
Phoca vitulina
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Phoca vitulina partial aar2B gene for alpha adrenergic
AJ251176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Madsen,O., Scally,M., Douady,C.J., Kao,D.J., Amrine,H.M., Stanhope,M.J., de Jong,W.W. and Parallel adaptive radiations in two major cla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (18-NOV-1999) Madsen O., Department of Biochemistry, University of Nijmegen, P.O. box 9101, 6500 HB Nijmegen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Madsen, O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 409 (6820), 610-614 (2001)
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Mammalia; Eutheria; Carnivora; Pinnipedia; Phocidae; Phoca.
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                                                  /Godon_start=2
/product="alpha adrenergic receptor 2B"
/db xref="agr:11122420"
/db xref="agr:11322420"
/db xref="agr:11122420"
/db xref="agr:11322420"
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/note="match to EST AA836522
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20537. .20973
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22057. .22471
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19266. .19675
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                                                                                                                                                                                                                                                                                                                                                                                                                           'gene="aar2B"
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mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'gene="aar2B"
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DEFINITION

Anomalurus exon 1.

ASP427259

1185 bp DNA linear ROD 25-OCT-200 sp. partial A2AB gene for alpha 2B adrenergic receptor.

ROD 25-OCT-2002

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (18-NOV-1999) Madsen O., Department of Biochemistry, University of Nijmegen, P.O. box 9101, 6500 HB Nijmegen, NETHERLANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aar2B gene; alpha adrenergic receptor
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AJ251177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sus scrofa (pig)
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                                                                                                                                                                                                                                              /db_xref="SPTREMBL:Q9GL06"
/translation="ALAAVITEFULLFTIFGNSLVILAVLTSRSLRAPQNLFLVSLAAA
/translation="ALAAVITEFULLFTIFGNSLVILAVLTSRSLRAPQNLFLVSWAVS
BILVATLILFSESLANBLLGYMVFRRTTWCEVYLLALDVLFCTSSIVHLCAISLDRYWAVS
RALEYNSKRTPRRIKCIILTVWLIAAVISLPPLIYKGDPGPOPRGRPQCKLNQEAWYI
LASSIGSFFAPCLIMILVYLRIYLIAXSHRROPRAKGGPKKGSKQPRRVPGEVSAS
AKLPTLVSQLATAGETNGCSQHTGEKDEGETSEBDTGTPAKLPEWPALPSSQGQCKEV
CGTSPEBBAEBEBECEPQTLPASPASACSPPLQQPQGSRVLATLRGQVLLGRGMGT
SGGQWWRRRAQLTREKKFTFVLAVVICTVFVLCWFPFFFFSYSLGAICPQHCKVPHGLF"
                                                                                                                                                                                                                                                                                                                                                                        /product="alpha adrenergic receptor 2B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic_DN
/db_xref="taxon:9823"
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                                                                                                                                                                                                                                                                                                                                                                                                                                          'gene="aar2B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Sus scrofa"
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AJ427259:1 GI:21655549
AJ427259:1 GJ:21655549
A2AB gene; alpha 2B adrenergic receptor.
Anomalurus sp.
Anomalurus gp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Anomaluridae;
                                                                                                                                                                                                                                                                                 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Huchon, D., Madsen, O., Sibbald, M.J., Ament, K., Stanhope, M.J., Catzeflis, F., de Jong, W.W. and Douzery, E.J.
Rodent phylogeny and a timescale for the evolution of Glires:
evidence from an extensive taxon sampling using three nuclear genes
Mol. Biol. Evol. 19 (7), 1053-1065 (2002)
                                                                                              complete sequence.
AL840630
AL840630.15 GI:31071445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (04-JAN-2002) Douzery E.J.P., Institut des Sciences de l'Evolution, Lab. Paleonto., Paleobio., Phylogenie, Universite
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cyprinidae; Danio.
1 (bases 1 to 149169)
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Zebrafish DNA sequence
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Douzery, E.J.P.
                                                       Danio rerio
                                                                   Danio rerio (zebrafish)
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Montpellier II,
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/number=1
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/protein id="CAD20297.1"
/db_xref="GI:21655550"
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/db_xref="taxon:101665"
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Pred. No. 72;
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regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Mi3 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em: RMBL; Sw: SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For
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Danio rerio clone RP71-44C4,
unordered pieces.
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Submitted (24-MAY-2003) Wellcome Trust Sanger Institute; Hinxton, Cambridgeshire, CB10 ISA, UK. E-mail enquiries:
zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on May 23, 2003 this sequence version replaced gi:30722485.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
                          Sims,
                                                                                                                                                                 BX510991.3 GI:31071389
HTG; HTGS PHASE1.
Danio rerio (zebrafish)
Danio rerio
Direct Submission
                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lloyd, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VECTOR: pTARBAC2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml
CH211-279L11 is from a CHORI-211 BAC library
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26273 c 26492 g 48515 t
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95.0%;
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Pred. No. 1.2e+C
O; Mismatches
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FEATURES
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Chemistry: Dye-terminator; 100% of reads
Consensus quality: 167404 bases at least Q40
Consensus quality: 168324 bases at least Q30
Consensus quality: 168018 bases at least Q20
Insert size: 170706; sum-of-contigs
Insert size: 189513; 3.5% error; agarose-fp
Quality coverage: 7.49x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On May 23, 2003 this sequence version replaced gi:30962299.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (21-MAY-2003) Wellcome Trust Sanger Institute, Hinxton,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: zfish-help@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                vector_side:left"
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ragment_chain:1"
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ragment_chain:1"
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ragment_chain:1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone_lib="RPCI-71"
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56699: gap of 100 bp
620679: contig of 5398 bp in length
621677: gap of 100 bp
887200: contig of 26553 bp in length
888200: gap of 100 bp
134708: contig of 45888 bp in length
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BASE COUNT
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                     S
                                                 Matches
                                                            Query Match
Best Local Similarity
                                                                                                                                                                           misc_feature
33134
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0; Mismatches 1.
                                                                                                               55051 t
                                                                                                               701 others
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Search completed: February 12, 2004, 04:41:51 Job time : 589.854 secs

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Minimum
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Perfect score:
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Gapop 10.0 , Gapext 1.0
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                                      2552756 segs, 1349719017 residues
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Human alpha-2B-adr Human alpha 2 beta	Human alpha-2B-adr Human alpha2B-adre Human alpha-2BAR t	Human alpha-2BAR g Human alpha2B-adre Human alpha-2BAR t	Description

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15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	16.4	16.4	16.4	16.4	16.4	16.4		16.8	16.8	16.8	17.4	17.4	. 20	20	20
79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	ö			ö	82.0	82.0	82.0		84.0	84.0	84.0	87.0	87.0	•	100.0	100.0
203	201	201	201	201	201	201	201	201	201	201	201	201	201	201	201	201	201	201	201	192	192	2944528	2944528	349980	4504	996	788	8902	2178	2177	1441	4910	965	3274	2072	2064
23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23		24	22	24	22	24	24	18	18	18	23	24	25	25	18
ABV01688	ABV14159	ABV12301	ABV10915	ABV10894	ABV10857	ABV10837	ABV10828	ABV10804	ABV10712	ABV10681	ABV10659	ABV10656	ABV04990	ABV01746	ABV01725	ABV01635	ABV01543	ABV01490	ABV01487	ABV40901	ABV31952	ABA03041	ABA03041	AAH68526	ABQ70977	AAH65708	ABQ68453	ABL51551	AAT48443	AAT48442	AAT48444	ABL03674	ABN98529	ABZ42624	ACA56583	AAT59499
prostate	prostate		prostate	prostate				Human prostate exp	Human prostate exp		prostate		prostate	prostate	prostate					Human prostate exp	Human prostate exp	Listeria monocytog	Listeria monocytog	C glutamicum codin	Listeria monocytog	C glutamicum codin	н		Human TGF-beta-lik		Human TGF-beta-lik	Drosophila melanog	Arabidopsis thalia	Human alpha 2b-adr	Human signalling p	Human alpha-2b adr

## ALIGNMENTS

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AAI99910
ID AAI9
XX AAI9
XX 18-F
XX 18-F
XX Huma
XX Huma
XX Cent
KW Huma
XX Cent
KW Phose
XX Homc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor; polymorphic site; allelic variant; cardiovascular disease; central nervous system disease; adenylyl cyclase; MAP kinase activity; phosphorylation; inositol phosphate; alpha-2BAR; PCR primer; ss.
Liggett SB,
                                                                                                                                                                                                                                                  17-APR-2000; 2000US-0551744.
10-AUG-2000; 2000US-0636259.
19-OCT-2000; 2000US-0692077.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200179561-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-APR-2001; 2001WO-US12575.
                                                                                              (LIGG/) LIGGETT S.B. (SMAL/) SMALL K M.
     Small KM;
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RESULT 2
AAD04761/c
ID AAD0477
XX AAD047
AC AAD047
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 10;
                                                                                                                                                                                                                                                                                                                                                                                                                norepinephrine; epinephrine; therapy; vascular contraction; coronary artery; coronary heat disease; CHD; chronic angina acute myocardial infarction; AMI; Prinzmetal's variant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; cardiant; gene therapy; alpha2B-adrenoceptor; alpha2B-AR; glutamic acid repeat; intracellular loop; chromosome 2; catecholamine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human alpha2B-adrenoceptor (alpha2B-AR) variant
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                                                                                                                                           /*tag= a
/product= "Human alpha2B-adrenoceptor (alpha2B-AR)
/product= "Human alpha2B-adrenoceptor (alpha2B-AR)
                                                                                                                                                                                                                                                                                         Location/Qualifiers
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WO200179561-A2

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is a gene encoding human alpha2B-adrenoceptor (alpha2B-AR) variant protein. Alpha2B-AR has a glutamic acid repeat element (amino acids 298-309) of 12 glutamates, in an acidic stretch of 18 amino acids (amino acids 294-311), located in the third intracellular loop of the receptor polypeptide. The variant is obtained by deletion of three glutamates from the Glu repeat (amino acids 307-309). Alpha2B-AR gene is located on chromosome 2. Alpha2-AR mediate many of the physiological effects of the catecholamines, norepinephrine and epinephrine. An antagonist of alpha2B-adrenoceptor is useful for treating a mammal suffering from vascular contraction of coronary arteries and a disease involving vascular contraction of coronary arteries which is clinically expressed as coronary heat disease (CHD), unstable chromic angina pectoris which is clinically expressed as Prinzmetal's variant form or acute myocardial infarction (AMI). Alpha2B-AR gene is used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Snapir A,
Scheinin N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New DNA molecule encoding variant specific adrenoceptor protein with deletion of specific amino acids located in the third intracellular loop of the polypeptide, for treating vascular contraction of coronary
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                                                                                                                                                                                        Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor; polymorphic site; allelic variant; cardiovascular disease; central nervous system disease; adenylyl cyclase; MAP kinase activity; phosphorylation; inositol phosphate; alpha-2BAR; chromosome 2; ds.
                                                                                                                                                                                                                                                                           Human alpha-2BAR third intracellular loop variant encoding
                                                                                                                                                                                                                                                                                                             18-FEB-2002
                                                                                                                                                                                                                                                                                                                                            AAI99906;
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                                                                                                               Location/Qualifiers
1..1344
                                 /product= "alpha-2BAR"
/note= "sequence is deleted for a 9 nucleotide
/note= polymorphic site found at nucleotides :
    of the wildtype alpha-2BAR protein (AA)
                                                                                                  *tag=
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Pred. No.
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T, Lakka
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Nyyssoenen
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RESULT 4
AAD44388/c
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AAC AAD44388;
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DT 13-DEC-200
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                                                                                                                                                                                                                                                                                                                                                                           The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic CC receptor gene (1) (III) by detecting a polymorphic site, comprising; CC (a) obtaining a sample having a polymorphic site, comprising; CC alpha2A or alpha2C or fragment or complement of; and CC (b) detecting a polymorphic site comprising nucleotide encoding an alpha-2B, CC (i) a site comprising (A) (yytosine or guanine at position 753 of (IIV) CC or a site comprising (Yotosine or guanine at position 753 of (IIV) CC or a site comprising (III). The method may be used for genotyping an CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine CC whether an individual is at increased risk of developing a disease associated with alpha2B, alpha2A or alpha2, comprising detecting a CC polymorphic site which correlate to disease selected from cardiovascular CC disease, central nervous system disease and combinations of these. In addition, the technique may be used to predict an individual's response CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epihephrine, CC norepinephrine, clonidine, oxymetazoline, younabenz, UK143104, BHT933 and CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239, rauwolscine, idazoxan, tolazoline, phentolamine and combinations of these) by detecting the polymorphic site and correlating the site to a predetermined response (where the response is correlated to adenylyl C cyclase, MAP kinase activity, phosphorylation or inssitol phosphate CC (Alays)905).

CC (Alays)905).
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Best Local S
Matches 20
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10-AUG-2000;
19-OCT-2000;
Human; hypertension; alpha-2B-adrenoceptor; AR; hypertension; hypotensive; variant; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for determining whether an individual is at increased risk of developing a disease associated with the corresponding receptor comprises detecting
                                                                                    13-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                           Sequence 1344
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(SMAL/)
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                                                 Human alpha-2B-adrenoceptor variant DNA.
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DB; AAM52118.
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SMALL K M.
                                                                                                                                                      standard;
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; 2000US-0636259.
; 2000US-0692077.
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Pred. No. 5.7
0; Mismatches
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                                                                                                                                                                                                                                                                                                                      5.7;
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                 antihypertensive;
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Best Local S
Matches 20
                                                                                                                                                                                              Human; cardiant; gene therapy; alpha2B-adrenoceptor; alpha2B glutamic acid repeat; intracellular loop; chromosome 2; cate norepinephrine; epinephrine; reservab; vascular contraction; coronary artery; coronary heat disease; CHD; chronic angina acute myocardial infarction; AMI; Prinzmetal's variant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     are useful
The kit is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detecting a risk of hypertension and targeting treatment
by determining the pattern of alleles encoding a variant
alpha-2-adrenoceptor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                  Human alpha2B-adrenoceptor (alpha2B-AR)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a method for detecting a risk of hypertension by determining the pattern of alleles encoding a variant alpha-2B-adrenoceptor (AR) protein. The methods and compositions of the invention are useful for detecting risks and targeting treatment for hypertension. The kit is also useful for selecting for clinical drug trials testing the anthypertensive effect of compounds. The present sequence is human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 24-26; 35pp; English
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)B; AAE26633.
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                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
/*tag= a
/product=
protein"
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protein"
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1..1344
                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 20; D
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                          "Human alpha2B-adrenoceptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  266 T; 0
                                                                                                                                                                                                                                                                                                                                               gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24;
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                                                                                                                                                                                                                                                                         alpha2B-AR;
2; catechol
                          (alpha2B-AR)
                                                                                                                                                                                                                                                                       catecholamine;
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RESULT 6
AA19905/c
ID AA1999
XX AA1999
AC AA1999
AC Human
DE Human
XX Human
XX Human
XX Centr
KW Polymc
KW Polymc
KW Ponospl
KW GenBai
XX Homo
XX Homo
XX Homo
XX FT CDS
FT CDS
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Best Local
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                                                                                                              Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor; polymorphic site; allelic variant; cardiovascular disease; central nervous system disease; adenylyl cyclase; MAP kinase activity phosphorylation; inositol phosphate; alpha-2BAR; GenBank Accession AF009500; chromosome 2; ds.
                                                                                                                                                                                                       Human alpha-2BAR third intracellular loop encoding DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is a gene encoding human alpha2B-adrenoceptor (alpha2B-AR) protein. Alpha2B-AR has a glutamic acid repeat element (amino acids 298-309) of 12 glutamates, in an acidic stretch of 18 amino acids (amino acids 294-311), located in the third intracellular loop of the receptor polypeptide. Alpha2B-AR gene is located on chromosome 2. Alpha2-AR mediate many of the physiological effects of the catecholamines, norepinephrine and epinephrine. An antagonist of eatherholamines norepinephrine and epinephrine. An antagonist of vascular contraction of coronary arteries and a disease involving vascular contraction of coronary arteries which is clinically expressed as coronary heat disease (CHD), unstable chronic angina pectoris which is clinically expressed as Prinzmetal's variant form or acute myocardial infarction (AMI). Alpha2B-AR gene is used in gene therapy.
                                                                                                                                                                                                                                                 18-FEB-2002
                                                                                                                                                                                                                                                                               AAI99905
                                                                                                                                                                                                                                                                                                          AA199905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1353 BP; 223 A; 459 C; 405 G; 266 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Snapir A, H
Scheinin M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 27-29; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New DNA molecule encoding variant specific adrenoceptor protein with deletion of specific amino acids located in the third intracellular loop of the polypeptide, for treating vascular contraction of coronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-OCT-2000; 2000WO-FI00913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (JUVA-) JUVANTIA PHARMA LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                 1140
                                                                                                  sapiens.
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20; Conserv
                                                                                                                                                                                                                                                                                                        standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heinonen P, , Salonen JT,
                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; ilarity 100.0%; Conservative 0
                                                                                                                                                                                                                                             (first entry)
/*tag= a
/product= "alpha-2BAR"
/note= "sequence includes
                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                       DNA; 1353
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                                                                                                                                                                                                                                                                                                     ВР
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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T, Lakka
a 9 nucleotide polymorphic
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                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
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Nyyssoenen
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13-DEC-2002 AAD44389; AAD44389

(first entry)

RESULT 7 AAD44389/c

standard;

DNA; 1353

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1140

1 AAAAACGCCAATGACCACAG

20

AAAAACGCCAATGACCACAG 1121

Query Match Best Local S Matches 20

Similarity

100.0%; ilarity 100.0%; Conservative 0

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Score 20; DB Pred. No. 5.7 0; Mismatches

5.7;

Length

1353;

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Gaps

0

224 A; 458 C; 405 G;

266 T; 0 other; DB 23;

20;

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CC The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic CC (a) obtaining a sample having a polymorphic site, comprising; CC (a) obtaining a sample having a polymorphic site, comprising; CC (b) detecting a polymorphic site complement of; and (b) detecting a polymorphic site comprising nucleotide positions 901-909 (c) of (I), a site comprising cytosine or guanine at position 753 of (IIV) (c) positions 961-972 of (III). The method may be used for genotyping an explanata, alpha2A or alpha2A, or alpha2
Sequence 1353 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to receptor gene (I)-(III) h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for determining whether an individual is at increased risk of developing a disease associated with the corresponding receptor comprises detecting a polymorphic site -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Page 144; 163pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAM52117.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (LIGG/)
(SMAL/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-APR-2000; 2000US-0551744.
10-AUG-2000; 2000US-0636259.
19-OCT-2000; 2000US-0692077.
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SMALL K
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>ა</u> დ
                                        (AAI99906).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       at nucleotides 901-909 variant (AAI99906)"
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Human alpha-2B-adrenoceptor gene

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AAQ14151/c
ID AAQ14151 standard; DNA; 2064 BP
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                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a method for detecting a risk of hypertension by determining the pattern of alleles encoding a variant alpha-2B-adrenoceptor (AR) protein. The methods and compositions of the invention are useful for detecting risks and targeting treatment for hypertension. The kit is also useful for selecting for clinical drug trials testing.
                                                       CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detecting a risk of hypertension and targeting treatment in a subject by determining the pattern of alleles encoding a variant alpha-2-adrenoceptor -
01-OCT-1991.
                                                                                                                                                             06-JAN-1992
                                                                                                                                                                                   AAQ14151;
                                                                                                                                                                                                                                                                                                                                                             Sequence 1353 BP; 223 A; 459 C; 405 G; 266 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                    alpha-28-adrenoceptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 27-29; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salonen J;
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                    US5053337-A.
                                                                                         Homo
                                                                                                               Neurotransmission;
                                                                                                                                     Human alpha 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; hypertension; alpha-2B-adrenoceptor; AR; antihypertensive; hypertension; hypotensive; gene; ds.
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                                                                                                                                                                                                                                                                   1140
                                                                                                                                                                                                                                                                                                                                                                                               antihypertensive effect of compounds. The present sequence is human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2002-667063/71.
DB; AAE26634.
                                                                                        sapiens
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                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                            (first entry)
                                                                                                                                      beta
                                         Location/Qualifiers
288..1752
/*tag= a
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                                                                                                              adrenaline;
                                                                                                                                     adrenergic
                                                                                                                                                                                                                                                                                                               100.0%; Score 20; DE 100.0%; Pred. No. 5.7 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    gene.
                                                                                                                                     receptor gene
                                                                                                              epinephrine; NGC-alpha2beta; ss
                                                                                                                                                                                                                                                                                                                           5.7;
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RESULT 9
AAT59499/c
ID AAT594
XX AAT594
XX AAT594
XX AAT594
XX 25-MAR
DT 06-MAY
XX 25-MAR
DT 06-MAY
XX epinep
XX Homo 8
XX Homo 8
XX Homo 8
XX US5595
XX US5595
XX US5595
XX 21-JAN
XX 21-JAN
XX 21-JAN
XX 22-OCT
XX 30-OCT
PR 30-MAY
PR 22-OCT
XX 30-MAY
PR 22-OCT
XX ASSAY
PN (SYNA-
XX HAFT1:
PA ASSAY
PT ASSAY
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Best Local S
Matches 20
                                                                                                               30-OCT-1989;
30-MAY-1991;
22-OCT-1992;
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                                                                                                                                                                                                                                                                                                                  Alpha-2b adrenergic receptor; adrenoceptor; adrenaline; epinephrine; signal transduction; neurotransmitter; ligand; ss.
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06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                       AAT59499;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-OCT-1989;
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                        WPI; 1997-107576/10.
P-PSDB; AAW11804.
                                                                                                                                                                                          21-JAN-1997
                                                                                                                                                                                                                                                                                                                                                       Human alpha-2b adrenergic receptor genomic DNA clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acids encoding alpha, 2-beta adrenergic receptor, for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAR14149.
                                                             Hartig
                                                                                                                                                                 22-OCT-1992;
                                                                                                                                                                                                                 US5595880-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated DNA encoding human adrenergic receptor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (NEUR-) NEUROGENETIC CORP.
                                                                                      (SYNA-) SYNAPTIC PHARM CORP
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                                                                                                                                                                                                                                                                                           sapiens
                                                             PR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
ilarity 100.0%;
Conservative 0
                                                              Weinshank
                                                                                                                                                                                                                                                                                                                                                                                (updated)
(first entry)
                                                                                                              89US-0428856.
91US-0707604.
92US-0965040.
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288:.1751
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               other;
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0;

Assay for alpha-2b adrenergic receptor ligands - using membranes

0f

cells expressing recombinant receptor

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RESULT 10
ACA56583/c
ID ACA565
XX ACA565
XX ACA565
XX Human
XX Human;
KW signal
KW signal
KW inmunc
XX Homo s
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YX US6500
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XX J-JAN
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XX J-JAN
XX J-JAN
XX G-Mbi
PR 30-JAN
XX Human;
XX G-Mbi
PR 30-JAN
XX G-Mbi
PR G-Mbi
PT Combi
PT G-Mbi
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Best Local
                                                        The invention relates to a combination which, comprises a number of polynucleotide probes comprising a sequence selected from one of the 1490 sequences mentioned in the specification. The combination is useful as an array element in a microarray for monitoring the expression of a number of target polynucleotides. The microarray is particularly useful in the diagnosis and treatment of cancer and immunopathology and neuropathology. The microarray is useful in diagnostics and treatment regimens, drug
                                                                                                                                                                                                                                                                                                                                                                                                                                        Combination of polynucleotide probes, useful as array elements in microarray for monitoring the expression of a number of target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; probe; ss; array element; Parkinson's disease; signalling pathway population; cancer; adenocarcinoma; leukaemia; immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; micro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A genomic DNA clone (AAT5949) codes for human alpha-2B adrenergic receptor (AAW11804), a member of the rhodopsin-like signal transduce family. It was isolated from a human spleen genomic library in the lambda vector Charon 2B by screening with a 1.6 kb fragment of the human 5-hydroxytryptamine receptor gene. Plasmid pNGC-alpha-2B comprising DNA encoding the alpha-2B adrenoceptor is deposited as ATCC 68144. Vectors have been adapted to allow prodn. of alpha-2B adrenoceptor in bacterial, yeast or mammalian cells; transfected Ltk- cells, designated L-NGC-alpha-2B, are deposited as ATCC CRL 10275. Membranes of such cells can used in novel methods to identify drugs which specifically interact with, and bind to, the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-352189/33.
                                                 discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Au-Young
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (INCY-) INCYTE GENOMICS INC
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                                             development,
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Matches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G protein-coupled receptor; GPCR; antigenic peptide; gene therapy; growth-related disease; cell regeneration-related disease; growth-related disease; cell regenerative disease; autoimmune disease; immunological-related cell proliferative disease; autoimmune disease; hlzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy; osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; graft versus host disease; Parkinson's disease; multiple sclerosis; pain; psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
                                                                                                                                                                                                                                                                                                                                                 Burmer GC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   forensics and pharmacogenomics. The microarray is also useful for monitoring progression of diseases and for developing sophisticated profiles for the effects of currently available therapeutic drugs. The combination is also useful for purifying a subpopulation of mRNAs, cDNAs and genomic fragments and in research and diagnostic applications. The array can detect changes in expression in a large number of genes coding for different signaling pathway populations which can be used to diagnose various diseases including cancer e.g. adenocarcinoma and leukaemia, immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease and Parkinson's disease. The present sequence represents a polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-DEC-2000; 2000US-257144P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-AUG-2002.
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New isolated antigenic peptides e.g., for G (GPCR), useful for diagnosing and designing conditions in which GPCRs are involved, e.g.

protein-coupled receptors.
drugs for treating
 AIDS, Alzheimer's disease

disease

autoimmune diseases Fig 1; 523pp;

ABP81780

Disclosure;

invention describes antigenic peptides

(I)

comprising

English.

CC (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino CC acids. Also described: (1) an assay for the detection of a particular CC G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; CC and (2) an isolated antibody having high specificity and high affinity or avidity for a particular GPCR. (1) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting CC antibody against a particular GPCR, and in the production of specific CC presence or absence of corresponding GPCRs. The antigenic peptides for CC GPCRs and antibodies are useful for disgnosing and designing drugs for CC regeneration-related diseases, growth-related designing drugs for CC gives and antibodies are useful for disgnosing and designing drugs for CC offices and antibodies are useful for disgnosing and designing drugs for CC elementation-related disease, immunological-related cell proliferative CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease, call constantivitis, osteoporosis, cancer, cardiomyopathy, chronic and acute inflammation, allergise, Crohn's disease, disease, disease, disease, disease, parkinson's disease, multiple sclerosis, pain, psoriasis, cancery, depression, schizophrenia, dementia, mental retardation, memory constantive, depression, schizophrenia, dementia, mental retardation, memory constantive, candiomyopathy, chronic and acute constantive, pain, psoriasis, cancery, cardiomyopathy, chronic and acute constantive, depression, schizophrenia, dementia, mental retardation, memory charactery, depression, schizophrenia, cancer, cardiomyopathy, chronic and cute constantive, depression, schizophrenia, dementia, mental retardation, memory charactery, depression, schizophrenia, cancer, cardiomyopathy, chronic and cute constantive, depression, schizophrenia, charactery, and mental retardation, memory charactery, and memory

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RESULT 12
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                                                                                                                                                                Arabidopsis thaliana; plant; insecticide; fungicide; transgenic; stress; disease; crop; thale cress; tolerance factor; insect; pathogen;
                                                                                                                                             Arabidopsis thaliana.
                                                                                                                                                                                    Arabidopsis thaliana expressed polynucleotide SEQ ID NO
                                                                                                                                                                                                 01-AUG-2002 (first entry)
                                                                                                                                                                                                                           ABN98529 standard; DNA;
                                                                                                                                                                                                                                                                                                                Sequence 3274 BP;
             (LEDF/
                          (PAGE/
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                                                          (PRIC,
                                                                       (GORL/)
                                                                                          27-JAN-2000; 2000US-178472P.
                                                                                                       26-JAN-2001; 2001US-0770445
                                                                                                                                                                                                               ABN98529;
                                       RAME/
                                                                HAMI/
                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                            1140 AMAMACGCCAATGACCACAG 1121
                                                                                                                                                                                                                                                                                      20;
                                                                                                                                                                                                                                                                         1 AAAAACGCCAATGACCACAG 20
           PAGE A.
MATHEW A V.
LEDFORD B L.
WOESSNER J P.
                                            HAMILTON C M.
PRICE J L.
RAINES T M.
YU Y.
HAAS W D.
GARCIA C A.
                                                                             GORLACH J.
                                      RAMEAKA J G.
                                                                       Ž
                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                              587 A; 979 C; 967 G; 741 T; 0 other;
                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                            965 BP
                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                      Score 20; DB
Pred. No. 6.3
0; Mismatches
                                                                                                                                                                                                                                                                                            6.3;
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                                                                                                                                                                                                                                                                                                  Length 3274;
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                                                                                                                                                                                    297.
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                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                      0
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RESULT 13 ABL03674

밁 S

219

2 AAAACGCCAATGACCACAG 20

Matches Best Local Query Match

18;

Conservative

0; Mismatches Pred. No. Score 17.4;

95; BB 24;

Length

965; 0,

Gaps

0

Similarity

87.0%; 94.7%;

Sequence 965 BP; 218 A; 314 C; 161 G;

268 T; 4 other;

# # # # #

ABL03674

ABL03674 standard; cDNA;

4910

ВP

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Comprising a sequence capable of hybridising under stringent conditions comprising a sequence selected from any one of 999 sequences (ABN99231), comprising an exequence selected from any one of 999 sequences (ABN99231), comprising an exequence selected from any one of 999 sequences (ABN99231), comprising an exequence sequence acid, is comprising an exequence sequence acid, is constituted by comprising an exequence sequence acid, is compressing an exequence sequence acid, is compressing an exequence sequence acid, is compression or sequence acid, is compression or control of its encoded compositions that modulate the expression or function of its encoded compositions that modulate the expression or function of its encoded compositions that modulate the expression or function of its encoded compositions that modulate the expression or function of its encoded compositions that modulate the expression or function of its encoded compositions that modulate the expression of protein and in studying associated physicological pathways. (I) is also useful in secreening compositions that complete acid, is series. (II) and (III) are useful for screening of biologically active compositions of the screened agents are useful in improved methods of treating crops to prevent or treat disease. (II) are also useful in screening compositions to identify sents that mind or enhance the action of tolerance companies to dentify sents that mind or enhance the action of tolerance companies to dentify agents that mind or enhance the action of tolerance compositions of mutritional product in a particular plant, (III) is useful in improved methods of treating crops to plant. (III) is useful for identifying other mediators that enhance or induce collection of the collular metabolism and for screening compounds constituted that the collular metabolism and for screening compounds constituted and control of the period of the printed constitution, but was obtained in electronic format directly from USPTO constitution and toleration of the perio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gorlach J,
Rameaka JG,
                                   specification, but was obtained in electronic format d
at seqdata.uspto.gov/sequence.html?DocID=999909770445.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New Arabidopsis thaliana nucleic acid for identifying homologous genes, producing compositions that modulate the expression or function of its encoded protein, and mapping functional regions of protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 297; 49pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-400781/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Garcia CA,
Hurban P;
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(SLAT/)
(DAVI/)
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SLATER T.
DAVIS K R.
ALLEN K.
HOFFMAN N.
HURBAN P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 An Y, Hamilton CM,
, Page A, Mathew AV,
Kricker M, Slater T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Price JL, Raince
Ledford BL, Woessner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Woessner JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hoffman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yu Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haas
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABL018737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                  pCL13; clone 13; transforming growth factor-beta; TGF-beta; immunosuppressive; cell differentiation; antiproliferative; wound healing; vulnerary; ischaemic injury; inflammation; cautoimmune disease; fibrotic disease; diagnosis; gene thera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid
genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
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                                                                                                                                                                               11-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4910 BP; 1279 A; 1083 C; 1134 G; 1414 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 5504; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pharmaceutical; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila; developmental biology; cell signalling; insecticide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAR-2002
                                                                                                                                                                                                                                   AAT48444 standard; cDNA; 1441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PEKE ) PE
                                                                                                                                                                                                                                                                                                                                                                                                                             ftp.wipo.int/pub/published_pct_sequences.
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DB; ABB59571.
                                                          sapiens
                                                                                                                                                   TGF-beta-like cytokine pCL13 variant
                                                                                                                                                                                                                                                                                                                                                    18;
                                                                                                                                                                                                                                                                                                                          1 AAAAACGCCAATGACCACA 19
                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                            (first entry)
                   Location/Qualifiers 234..1160
                                                                                                                                                                                                                                                                                                                                                              87.0%;
94.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                .1e+02
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                                                                                    gene therapy;
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                                                                                                  cancer;
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RESULT 15
AAT48442C
ID AAT484
AX AAT484
AX AAT484
XX INMAN IN-APR
XX PCL13;
XX pCL13;
XX inmunoo
KW inmunoo
KW autoim
XX wound autoim
XX Homo s
XX Homo s
XX Key
FT CDS
XX KO9700
XX WO9700
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           novel TGF-beta-like cytokine whose activities include immunosuppression, down-regulation of leucocyte extravasation and motility, promotion of cell differentiation and inhibition of proliferation. The clones were obtd. from a foetal lung library using a portion of the coding region of clone 13 (see also AAT48438) as probe. They show substantial variation in the 5' untranslated region but only minor differences in the coding region. Translated coding regions are given in AAW10666-73. While the variants may be important in e.g. transcriptional reglation they are untranslated and hence cannot affect bioactivity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-FEB-1996;
22-JUN-1995;
23-AUG-1995;
                                                                                                                                pCL13; clone 13; transforming growth factor-beta; TGF-beta; immunosuppressive; cell differentiation; antiproliferative; wound healing; vulnerary; ischaemic injury; inflammation; c autoimmune disease; fibrotic disease; diagnosis; gene thera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated nucleic acid encoding pCL13, new TGF-beta family member has immunosuppressant, cell differentiation promoting and anti:proliferative activities, for treatment of wounds, ischaemic injury, cancer, inflammatory disease etc.
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                                                                                                                                                                                                                                  11-APR-1997
                                                                                                                                                                                                                                                                AAT48442
                                                                                                                                                                                                                                                                                         AAT48442 standard; cDNA; 2177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1441 BP; 300 A; 451 C; 428 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA clones b2, h1, u2, f1, a1, b1, d2 variants of clone 13 (AAT48438), which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 17; Fig 20A; 73pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bootcov M,
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                                                                                                    Homo sapiens
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                                                                                                                                                                                                       TGF-beta-like
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95AU-0003706.
95AU-0004990.
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                                                       Location/Qualifiers
993..1919
                                                                                                                                                                                                     cytokine pCL13 variant
                                                                                                                                                                                                                                  entry)
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90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 16.8; DB 18
Pred. No. 1.9e+02;
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                                                                                                                                                 cancer;
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0;

WO9700958-A1

09-JAN-1997.

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                                                                                                                                                Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-FEB-1996;
22-JUN-1995;
23-AUG-1995;
                                                                                                                                                                                                                                                         cDNA clones b2, h1, u2, f1, a1, b1, d2 and dd2 (AAT48442-49) are variants of clone 13 (AAT48438), which codes for pCL13 (AAW10662), a novel TGF-beta-like cytokine whose activities include immunosuppression, down-regulation of leucocyte extravasation and motility, promotion of cell differentiation and inhibition of proliferation. The clones were obtd. from a foetal lung library using a portion of the coding region of clone 13 (see also AAT48438) as probe. They show substantial variation in the 5 untranslated region but only minor differences in the coding region. Translated coding regions are given in AAW10666-73. While the variants may be important in e.g. transcriptional reglation they are untranslated and hence cannot affect bioactivity.
                                                                                                                                                                                                                        Sequence 2177 BP; 462 A; 645 C; 609 G; 461 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 17; Fig 20A; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated nucleic acid encoding pCL13, new TGF-beta family member - has immunosuppressant, cell differentiation promoting and antiproliferative activities, for treatment of wounds, ischaemic injury, cancer, inflammatory disease etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bootcov M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-JUN-1996;
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                                                                       869 AAACACTCCAATGACCACAG 850
                                                                                                1 AAAAACGCCAATGACCACAG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Breit S;
                                                                                                                                              84.0%; Score 16.8; DB 18; Length 2177; ilarity 90.0%; Pred. No. 2e+02; Conservative 0; Mismatches 2; Indels 0;
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95AU-0003706.
95AU-0004990.
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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seq length: 2000000000
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Match Length DB
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| cgn2_6/ptodata/2/ina/5A_COMB.seq:*
| cgn2_6/ptodata/2/ina/5B_COMB.seq:*
| cgn2_6/ptodata/2/ina/6B_COMB.seq:*
| cgn2_6/ptodata/2/ina/6B_COMB.seq:*
| cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
| cgn2_6/ptodata/2/ina/backfiles1.seq:*
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SUMMARIES
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Sequence 130, App
Sequence 1673, Ap
Sequence 312, App
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     3388 Appli
3388 Appl
76, Appl
76, Appl
1004, Ap
1004, Appli
7, Appli
8, Appli
8, Appli
8, Appli
9, App
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4, Appli
3, Appli
103, App
106, App
6186, App
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45	44	43	42	41	40	9	38	37	36	35	34	33	32	31	30	29	28
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71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0	72.0	72.0	72.0
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US-08-945-848-7	US-09-397-787-157	US-09-107-532A-3178	US-08-911-020-4	US-08-341-568-4	US-09-328-352-1188	US-09-134-001C-2780	US-09-328-352-937	US-07-661-610C-12	US-09-134-001C-2684	US-09-134-001C-2032	US-09-313-294A-885	US-09-107-532A-583	US-09-134-001C-2061	US-09-313-294A-1872	US-09-417-381A-8	US-08-440-816A-8	US-08-441-104A-8
Sequence 7, Appli	Sequence 157, App	Sequence 3178, Ap	Sequence 4, Appli	Sequence 4, Appli	Sequence 1188, Ap	Sequence 2780, Ap	Sequence 937, App		Sequence 2684, Ap	Sequence 2032, Ap	Sequence 885, App	Sequence 583, App	Sequence 2061, Ap	Sequence 1872, Ap	Sequence 8, Appli	Sequence 8, Appli	Sequence 8, Appli

## ALIGNMENTS

RESULT 1 US-09-016-434-1181/c

GENERAL INFORMATION:

1181, Application US/09016434 5. 6500938

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CLONE: GENBANK
US-09-016-434-1181
Query Match
Best Local Similarity
                                                                                                                                                                          TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2072 base pairs
                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEPAX: (650) 845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Janice Au-Young .
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
                                                                                   IMMEDIATE SOURCE:
LIBRARY: GENBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: HEREW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: INCYTE PHARMACEUTICALS, INC
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
                                                                                                                      STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                         TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
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                Length 2072;
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              GENERAL INFORMATION:
APPLICANT: LYTH DOUGETTE-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
                                                                                           Sequence 1673, Application US/09134001C Patent No. 6380370
                                                                                                                                                                                                                                                         Matches
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   CURRENT APPLICATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE:
ORGANISM: MYCOBACTERIUM LEPRAE
                                                                                                                                                                                                                                                                                                                                                                    MOLECULE NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION UMBER: 31,616
REFERENCE/DOCKET NUMBER: CO
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: doubt
TOPOLOGY: circular
MOLECULE TYPE: DNA (
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TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                          Local
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENGTH:
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                                                                                                                                                                                            26433 ACGCCAATGACCACAG 26448
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                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/08311731A
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NUMBER: US/09/134,001C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 312, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/09029213B Patent No. 6180098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 312
LENGTH: 1779
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SEQ ID NO 1673
LENGTH: 1593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Best Local :
                                                                                                                                                                                                                                                                                                                                                             GENERAL
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PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 8252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: GTC99-03PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                  APPLICANT: CHRISTIAN TITLE OF INVENTION: 1 TITLE OF INVENTION: 1 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CLASSIFICATION:
              APPLICATION NUMBER: US/0 FILING DATE: 31-AUG-1998
                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                 STATE:
                                                                                                                                                                                                              CITY: Washington
                                                                                                                                                                                                                                                   ADDRESSEE:
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                                                                                                                                                                                             District of Columbia
                                                                                                                                                                                                                              600 13th Street,
                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                          CHRISTIAN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76.0%; ilarity 85.0%; Conservative
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                                                                                                                                                                                                                                                                                                   RECOMBINANT HELICOVERPA BACULOVIRUSES EXPRESSING HETEROLOGOUS DNA
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                                 US/09/029,213B
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Pred. No. 1.4e+02;
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Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1779;
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ATTORNEY/AGENT INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPHONE:

NAME: Joseph Hyosuk Kim REGISTRATION NUMBER: 41,425 REFERENCE/DOCKET NUMBER: 50

50179-048

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US-08-931-999-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-029-213B-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                              Description US/08931999
Patent No. 6043219
                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 202-756-8087 INFORMATION FOR SEQ ID NO:
                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                  APPLICANT: Iandolo, John J.
APPLICANT: Crupper, Scott S.
TITLE OF INVENTION: Broad Spectrum Chemotherapeutic
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 5820 base pairs
TYPE: nucleic acid
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EATURE:
                                                                                                                                                                                            ADDRESSEE: Hovey, Williams, T. STREET: 2405 Grand Boulevard, CITY: Kansas City
                            PILING DATE:
CLASSIFICATION:
                                                          APPLICATION NUMBER:
                                                                                                                                                           ZIP: 64108
                                                                                                                                                                    COUNTRY:
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                                                                                                                                                                     Missouri
Y: U.S.A.
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1388..1973
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85.0%;
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Pred. No. 1.7e
0; Mismatches
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d, Suite 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 3
LENGTH: 55827
TYPE: DNA
ORGANISM: Human
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Matches
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Matches
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GENERAL INFORMATION:
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GENERAL INFORMATION:
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                  APPLICANT: Leppert, Mark F.
APPLICANT: Singh, Nanda
APPLICANT: Singh, Nanda
APPLICANT: Charlier, Carcle
TITLE OF INVENTION: KCNQ2 AND KCNQ3 - POTASSIUM CHANNEL GENES WHICH ARE
TITLE OF INVENTION: MUTATED IN BENION FAMILIAL NEONATAL CONVULSIONS (BFNC)
TITLE OF INVENTION: AND OTHER EPILEPSIES
FILE REPERRNCE: 2323-134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/813,133A
CURRENT FILING DATE: 2001-06-06
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: CL001173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: GAN, Weiniu et al
CURRENT APPLICATION NUMBER: US/09/177,650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 6755 base pair
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ATTORNEY/AGENT INFORMATION:
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mes 17; Conserv
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17; Conserv
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DEDNESS: double
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Pred. No. 2.5e+02;
0; Mismatches 3;
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Pred. No. 1.8e+02;
0; Mismatches 3;
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APPLICANT: Xu, Jiangchun
ITITLE OF INVENTION: COMPOUNDS AND METHODS FO
ITITLE OF INVENTION: OF COLON CANCER
FILE REFERENCE: 210121.471
CURRENT APPLICATION NUMBER: US/09/221,298
CURRENT FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 106
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US-09-221-298-106
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; ORGANISM: Homo sapiens
US-09-177-650-103
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NAME/KEY: modified_base
LOCATION: (18)
OTHER INFORMATION: Where n
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EARLIER APPLICATION NUMBER: 60/063,147
EARLIER FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 129
SOFTWARE: PACENTIN VEY. 2.0
SEQ ID NO 103
LENGTH: 215
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Best Local Similarity
                                            LOCATION: (219)
OTHER INFORMATION: Where
                                                                  NAME/KEY: modified_base
                                                                                                                NAME/KEY: modified_base
 OTHER INFORMATION: Where
                NAME/KEY: modified_base
LOCATION: (247)
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OTHER INFORMATION: Where
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OTHER INFORMATION: Where n
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OTHER INFORMATION: Where n
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RESULT 11
US-08-169-715-1/c
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; LOCATION: 264, 286
; OTHER INFORMATION: a,
US-09-313-294A-6186
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SOFTWARE: PEKE
SEQ ID NO 6186
TENGTH: 291
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GENERAL INFORMATION:
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APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYMUCLEOTIDES AND POLYPEPTIDES DERIVED FILE REFERENCE: PL-0017 US CURRENT APPLICATION NUMBER: US/09/313,294A CURRENT FILING DATE: 1999-05-14 NUMBER OF SEQ ID NOS: 7600 SOFTMARE: PERL Program
SOFTMARE: PERL Program
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                                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 29
TYPE: DNA
                                   APPLICANT: Irvine, Bruce D.
APPLICANT: Horn, Thomas
APPLICANT: Chang, Chu-An
TITLE OF INVENTION: HIV PROBES FOR USE IN SOLUTION PHASE
TITLE OF INVENTION: SANDWICH HYBRIDIZATION ASSAYS
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
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NAME/KEY: modified_base

TOTATION: (255)

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OTHER INFORMATION: Where n is
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SEE: Morrison & Foerster
1: 545 Middlefield Road, Suite
Menlo Park
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RESULT 13
US-09-661-596A-76/c
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; Patent No. 6528066
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                                                                                                                                                                                                                                                                            ; TYPE: DNA ; ORGANISM: Acinetobacter baumannii US-09-328-352-3388
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US-09-328-352-3388/c
                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 3388
LENGTH: 1422
                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3388, Application US/09328352 Patent No. 6562958
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REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 2230
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEPAX: 415-327-2951
APPLICANT: Grose, Charles
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/169,715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 07/8
FILING DATE: 18-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Local Similarity 66.7%;
es 8; Conservarivo
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                 INFORMATION:
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88.9%;
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Pred. No. 2
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Pred. No. 1
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LENGTH: 1788
TYPE: DNA
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APPLICANT: GATY L. Breton et al.
APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn version 3.0 SEQ ID NO 76
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CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/153,779 PRIOR FILING DATE: 1999-09-14
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TITLE OF INVENTION: VARIANT VARICELLA-ZOSTER VIRUSES AND METHODS OF USE
FILE REFERENCE: 140.0011 0101
                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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TYPE: DNA
ORGANISM: Varicella zoster
                                                                                                                                                                                                                                                                                                                        quence 7, Appli
tent No. 584409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Acinetobacter baumannii
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb f
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                            APPLICANT: Presta, Leonard G.
APPLICANT: Shelton, David L.
APPLICANT: Urfer, Roman
TITLE OF INVENTION: Human trk Receptors and Neurotrophic Factor Inhibitors
NUMBER OF SEQUENCES: 41
                                                                                                                                                                                             CORRESPONDENCE ADDRESS
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                                                                                                                                        Francisco
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88.9%;
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Pred. No. 3.5e+02;
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Pred. No. 4
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CURRENT APPLICATION NUMBER: US/08/359,705B

PILING DATE: 09/08-1994

CLASSIFICATION: 424

PRIOR APPLICATION UMBER: 08/286846

PRIOR APPLICATION NUMBER: 08/286846

PRIOR APPLICATION NUMBER: 08/215139

PRIOR APPLICATION NUMBER: 08/21513

PRIOR APPLICATION NUMBER: 08/215139

PRIOR APPLICATION NUMBER: 08/21513

PRIOR APPLICATION NUMB
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Database :
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Maximum Match 100%
Listing first 45 summaries
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seq length: 2000000000
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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1282	996	788	2965	3274	2072	1353	1353	1353	1344	1344	1344	20	Length
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US-10-017-161-2099	US-09-738-626-743	US-10-398-221-1266	US-09-770-445-297	US-10-225-567A-41	US-10-305-720-1181	US-10-001-073-1	US-10-077-870-3	US-09-825-923-3	US-10-001-073-2	US-10-077-870-1	US-09-825-923-1	US-10-001-073-16	ID
Sequence 2099, Ap		Sequence 1266, Ap	Sequence 297, App	Sequence 41, Appl	11	Sequence 1, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 16, Appl	Description

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US-10-312-841-2	US-10-312-841-1	US-10-398-221-2058	US-10-398-221-9	US-10-311-455-980	US-10-225-567A-43	US-09-938-842A-4905	US-09-938-842A-4905	US-10-101-510-450	US-10-001-073-40	US-10-001-073-42	US-10-447-328-31	US-10-369-493-37126	US-10-191-803-211	US-10-027-632-298548	US-10-027-632-298547	US-10-027-632-83957	US-10-027-632-83956	US-10-027-632-298548	US-10-027-632-298547	US-10-027-632-83957	US-10-027-632-83956	US-10-027-632-156513	US-10-027-632-156512	US-10-027-632-156513	US-10-027-632-156512	US-10-027-632-156514	US-10-027-632-156514	US-09-738-626-1	US-10-398-221-3790
Sequence 2, Appli	Sequence 1, Appli	Sequence 2058, Ap	ø	Sequence 980, App	Sequence 43, Appl	``	Sequence 4905, Ap	450	40,	42,	31,	Sequence 37126, A	Sequence 211, App			Sequence 83957, A	Sequence 83956, A	Sequence 298548,	Sequence 298547,	Sequence 83957, A	Sequence 83956, A	Sequence 156513,	Sequence 156512,	Sequence 156513,	Sequence 156512,	Sequence 156514,	Sequence 156514,	Sequence 1, Appli	Sequence 3790, Ap

## ALIGNMENTS

RESULT 1

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; Sequence 1, Application US/09825923; Patent No. US20010016338A1; GENERAL INFORMATION: APPLICANT: Snapir, Amir APPLICANT: Heinonen, Paula APPLICANT: Alhopuro, Pia APPLICANT: Karvonen, Matti APPLICANT: Koulu, Markku
                                                                                                                                                                                                                                                                                                                                                                                                             ; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-001-073-16
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US-09-825-923-1/c
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Publication No. US20030113725A1

GENERAL INFORMATION:
APPLICANT: Liggett, Stephen
APPLICANT: Small, Kirsten
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REFERENCE: 13073-PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-001-073-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/001,073
CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 20; DB Best Local Similarity 100.0%; Pred. No. 5.6; Matches 20; Conservative 0; Mismatches
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; NAME/KEY: CDS
; LOCATION: (1)..(1341)
; OTHER INFORMATION: Coding sequence for variant human alpha-2B-adrenoceptor protein
US-10-077-870-1
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US-10-077-870-1/c
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Publication No. US20030003470A1
GENERAL INFORMATION:
APPLICANT: Salonen, Jukka T
TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
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                                                                                                                  Query Match
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APPLICANT:
APPLICANT:
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CURRENT APPLICATION NUMBER: US/10/077,870
CURRENT FILING DATE: 2002-05-21
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APPLICANT: Valkonen, Veli-Pekka
APPLICANT: Valkonen, Veli-Pekka
TITLE OF INVENTION: A DUA molecule encoding a variant alpha-2B-adrenoceptor
TITLE OF INVENTION: protein, and uses thereof
FILE REFERENCE: Alpha-2B-AR variant
CURRENT APPLICATION NUMBER: US/09/825,923
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 09/422,985
PRIOR APPLICATION NUMBER: 09/422,985
PRIOR FILING DATE: 2000-05-25
NUMBER: CEC. IN NOC. 10
                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: FI 20010323
PRIOR FILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 10
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TYPE: DNA
ORGANIEM: Homo sapiens
FEATURE:
FEATURE:
LOCATION: (1)..(1341)
OTHER INFORMATION: Coding sequence for variant human
OTHER INFORMATION: alpha-2B-adrenoceptor protein
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                                                                                                                                                                                                                                                              LENGTH: 1344
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                   Local Similarity
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1131 AAAAACGCCAATGACCACAG 1112
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                                      1 AAAAACGCCAATGACCACAG 20
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Salonen, Riitta
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nilarity 100.0%;
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RESULT 4 US-10-001-073-2/c

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NAME/KEY: CDS
LOCATION: (1)..(1350)
COTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor
COTHER INFORMATION: protein
US-09-825-923-3
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LENGTH: 1344
TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT: Liggett, Stephen
APPLICANT: Small, Kirsten
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REFERENCE: 13073-PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Snapir, Amir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09825923 Patent No. US20010016338A1
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                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Kauhanen, Jussi
APPLICANT: Valkonen, Vali-Pekka
APPLICANT: Valkonen, Vali-Pekka
TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
TITLE OF INVENTION: Protein, and uses thereof
FILE REFERENCE: Alpha-2B-AR variant
CURRENT APPLICATION NUMBER: US/09/825,923
CURRENT FILING DATE: 2001-04-05
PRIOR FILING DATE: 2001-04-05
PRIOR FILING DATE: 2001-05-25
RIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/001,073
CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
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                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
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1140 AAAAACGCCAATGACCACAG 1121
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                                                                                            Similarity
                           AAAAACGCCAATGACCACAG
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Alhopuro, Pia
Karvonen, Matti
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Salonen, Riitta
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Scheinin, Mika
Salonen, Jukka T
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                                                                          Conservative
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Pred. No.
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Pred. No.
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-001-073-1
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US-10-001-073-1/c
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                                                                                                     Sequence 1181, Application US/10305720 Publication No. US20040010136A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Liggett, Stephen
APPLICANT: Small, Kirsten
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REFERENCE: 13073-PCT
CURRENT APPLICATION NUMBER: US/10/001,073
CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/10001073 Publication No. US20030113725A1 GENERAL INFORMATION:
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Publication No. US20030003470A1
GENERAL INFORMATION:
APPLICANT: Salonen, Jukks T
TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
FILE REFERENCE: 0933-0183P
                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expressi-
FILE REFERENCE: PA-0002-1 CON
CURRENT APPLICATION NUMBER: US/10/305,720
CURRENT FILING DATE: 2002-11-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: FI 20010323
PRIOR FILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 10
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CURRENT FILING DATE: 2002-05-21
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ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: (1)..(1350)
OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor protein
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100.0%; Pred. No. 8.
tive 0; Mismatches
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; LENGTH: 2072
; TYPE: DNA
; ORGANISM: Homo sapiens
; PEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: GenBank ID No. US20040010136A1 g178197
US-10-305-720-1181
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NUMBER OF SEQ ID NOS: 1490
SOFTWARE: BERL Program
SEQ ID NO 1181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 41
LENGTH: 3274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 41, Application US/10225567A Publication No. US20030113798A1
                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                              Sequence 297, Application US/09770445 Patent No. US20020023281A1
                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local (
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Burmer, Glenna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: LifeSpan Biosciences APPLICANT: Brown, Joseph P.
                                                                                                                                  APPLICANT
                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn version 3.1
                                                                                                                 APPLICANT
                                                                                                                                                APPLICANT
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                                                                                                                                                                                APPLICANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                             1140 AAAAACGCCAATGACCACAG 1121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1552 AAAAACGCCAATGACCACAG 1533
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                               Matthew, Abraham V.
Ledford, Brooke L.
Woessner, Jeffrey P.
Haas, William David
Garcia, Carlos A.
Kricker, Maja
Slader, Ted
                                                                                                                        Yu, Yang
Rameaka, Joshua G.
                                                                                                                                                                             Hamilton, Carol M.
Price, Jennifer L.
                                                                                                                                                                                                                            Gorlach, Jorn
                                                                                                               Page, Amy
                                                                                                                                                               Raines,
                                                                                                                                                                                                             An, Yong-Qiang
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ilarity 100.0%;
Conservative (
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Pred. No. 8.7;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 15;
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APPLICANT: Hoffman, Neil
APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: thaliana
FILE REFERENCE: 2023US (PARA-012PRV)
CURRENT APPLICATION NUMBER: US/09/770,445
CURRENT FILLING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: US 60/178,472
PRIOR FILLING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSEO F-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(965)
; OTHER INFORMATION: n = A,T,C or
US-09-770-445-297
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                                                       Sequence 1266, Application US/10398221
Publication No. US20040018514A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                             Query Match
Best Local 9
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SEQ ID NO 42551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)B CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
CURRENT FILING DATE: 2003-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
APPLICANT: KUNST, Frederik
APPLICANT: GLASER, Philippe
TITLE OF INVENTION: Listeria innocua, genome and applications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/360,039 PRIOR FILING DATE: 2002-02-21
                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Anabaena PCC7120
                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1767
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94.7%;
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90.0%;
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Pred. No. 2.8e+02;
0; Mismatches 2;
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Pred. No. 1
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RESULT 14 US-10-292-798-1745/c

Sequence 1745, Application US/10292798
Publication NO. US20030235833A1
GRMERAL INFORMATION:
APPLICANT: SUWA, MAKIKO

APPLICANT:

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NUMBER OF SEQ ID NOS: 7059

SOFTWARE: PatentIn ver. 3.0

SEQ ID NO 743

LENGTH: 996
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                                                                                                                                ; TYPE: DNA ; ORGANISM: Corynebacterium glutamicum US-09-738-626-743
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US-09-738-626-743/c
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; ORGANISM: Listeria monocytogenes-4B
US-10-398-221-1266
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 1266
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                                                                              Query Match
Best Local
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                 APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKTO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
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APPLICANT:
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PRIOR FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: FR 00/12 697
PRIOR FILING DATE: 2000-10-04
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CURRENT APPLICATION NUMBER: US/10/398,221
CURRENT FILING DATE: 2003-03-27
                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: JP 00/280988 PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: NAKAGAWA, SATOSHI
                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: JP 99/377484
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319 AAATGCCAATGACCACAG
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                             3 AAACGCCAATGACCACAG 20
                                                                                Similarity
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HAYASHI, MILL.
OCHIAI, KEIKO
OWOI, HARUHIKO
NAOKO
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SENOH, AKIHIRO
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o. US20020197605A1
                                                                  Conservative
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                                                                                82.0%;
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302
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                                                                                Score 16.4; DB 1
Pred. No. 4.1e+02
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                                                                  Mismatches
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APPLICANT: SUMA, MAXIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: ASAI, KIYOSHI
APPLICANT: ASAI, KIYOSHI
APPLICANT: ASURATMAN, YUTAKA
APPLICANT: ASURATMAN; HIROYUKI
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REPERENCE: 084335/0152
CURRENT APPLICATION NUMBER: US/10/017,161
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: JP 2001/246789
PRIOR PILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430
SOFTWARE: PACENTIN VET. 2.1
SEQ ID NO 2099
LENGTH: 1282
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                                                                                                                                                                                               ; NAME/KEY: CDS
; LOCATION: (201)..(1082)
US-10-017-161-2099
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US-10-017-161-2099/c
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; NAME/KEY: CDS
; LOCATION: (201)..(1082)
US-10-292-798-1745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 82.0%; Score 16.4; DB 12; Length 1282; Best Local Similarity 94.4%; Pred. No. 4.2e+02; Matches 17; Conservative 0; Mismatches 1; Indels 0;
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SEQ ID NO 1745
                                                                                               Query Match 82.0%; Score 16.4; DB 13; Length 1282; Best Local Similarity 94.4%; Pred. No. 4.2e+02; Matches 17; Conservative 0; Mismatches 1; Indels 0;
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APPLICANT: ABURATANI, HIROYUKI
APPLICANT: ABURATANI, HIROYUKI
TITLE OR INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
FILE REFERENCE: 084335/166
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US/10/292,798
PRIOR APPLICATION NUMBER: 10/017,161
PRIOR FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: JP 2001-246789
PRIOR APPLICATION DATE: 2001-06-18
NUMBER: OF SEQ ID NOS: 2070
                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SOURCE
LOCATION: (1)..(1282)
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
LOCATION: source
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LOCATION: (1)..(1282)
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1071 ACAACGCCAATGACCACA 1054
1071 ACAACGCCAATGACCACA 1054
                                2 AAAACGCCAATGACCACA 19
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Search completed: February 12, 2004, 06:16:00

Job time : 122.659 secs

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Maximum Match 100%
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Perfect score:
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                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                           Score |
19
18.4
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947076	BG5498	10	405	2	16.4	38
AI859458 wm12a08.x	>	9	355	٥	σ	37
BG549263 947074A07	BG54926	10	143		ð	36
BG910723 602809750	BG91072	12	1336	4	•	35
BH167326 ENTTF94TF		28	1115	4.	٠,	34
BG440575 GA_Ea000	BG440575	10	926	4	16.8	33
AL151283 Anopheles		29	916	4.	٠,	32
BZ203770 CH230-436		29	896	Α.	٠,	31
AL311552 Tetraodo		29	889		٥,	30
AL606568 Sea Hors		29	882	4.	٠,	29
60305825	BI768763	12	878	4	σ	28
		28	858	4.	ა	. 27
		13	855	4.	٥.	26
Zebrafis		29	788	4.	٥,	25
AZ907242 RPCI-24-1	AZ90724	28	765			24
CB630921	CB630921	14	742	4.		23
AI055134	AIOS	9	729	4.	σ	22
CB677776 OSJNEe15	CB677776	14	722	4.		21
AZ352444	AZ352444	28	. 668	4		20
BQ109472 imageqc	BQ109472	13	658	4.	٠	19
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UI-E-CI1	BM690995	12	513	Α.	•	16
G143944 T	G143	10	500	4.	٥,	15
3573 qu	AI243573	9	445	4.	٥,	14
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395866 MA000059	395866	9	7	4	16.8	7
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96 601811	BF129496	10	1752		17.4	ຫ

## ALIGNMENTS

		92.0 986			Match Length	Query	40
29	9	10	29		DB I		
CNS07D83	1993504	BE788667	HGRA2BAR		٥		
AL440137 T3 end of	AI993504 701496517	BE788667 601475536	AL606572 Shark alp		Description		
		source	FEATURES			JOURNAL	TITLE
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	source	FEATURES		JOURNAL	TITLE	AUTHORS	REFERENCE	JOURNAL	TITLE	AUTHORS	REFERENCE				ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	Locus	RESULT 1 HGRA2BAR/c	
/organism="Hexanchus griseus" /mol_type="genomic DNA"	1712	biohelp@hgmp.mrc.ac.uk Location/Qualifiers	Centre Hinxton, Cambridge, CB10 1SB. UK Email:	Submitted (14-SEP-2001) MRC Human Genome Mapping Project Resource	Direct Submission	Hunter, C.	2 (bases 1 to 712)	Unpublished	Alpha2 adrenergic receptor gene	Hunter, C. and Elgar, G.	1 (bases 1 to 712)	Hexanchoidei; Hexanchidae; Hexanchus.	Elasmobranchii; Squalea; Notidanoidea; Hexanchiformes;	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;	Hexanchus griseus	Hexanchus griseus	GSS; Alpha2 adrenergic receptor gene.	AL606572.1 GI:15591923	AL606572	genomic survey sequence.	Shark alpha2 adrenergic receptor gene fragment probably subtype b,	HGRA2BAR 712 bp DNA linear GSS 14-SEP-2001		

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 986)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
BE788667
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Tissue Procurement: DCTD/DTP/Gazdar
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Mammalia; Eutheria; Primates;
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Plate: LLAM9642 row: g column: 10
High quality sequence stop: 254.
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                                      AI993504 527 bp mRNA linear EST 08-SEP-1701496517 A. thaliana, Ohio State clone set Arabidopsis thaliana CDNA clone 701496517, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             found through the I.M.A.G.E. Consortium/LLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. clone distribution: MGC clone distribution information can be
             AI993504
AI993504.1 GI:5840409
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                                                                                                                                                                                                                                                                /clone="IMAGE:3878433"
/tissue_type="large_cell_carcinoma"
/lab host="DH10B (phage_resistant)"
/clone_lib="NIH MGC_68"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Not1;
/note="Organ: lung; Vectorionally. Primer: Oligo dr. Site_2: Sall; Cloned unidirectionally. Primer: Oligo dr. Average_insert_size_1.8 kb. Library constructed by Life Technologies."
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/mol_type="mRNA"
/db_xref="taxon:9606"
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1 (bases 1 to 527)
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Location/Qualifiers
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Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Kalgeropoulos, O., Potier, S.,
Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)
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1 (bases 1 to 971)
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T3 end of clone BD0AA010C06 of library BD0AA from strain CBS
Candida tropicalis, genomic survey sequence.
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tropicalis
FEBS Lett. 487
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Blandin,G., Ozier-Kalogeropoulos,O.,
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314-427-3324
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/clone lib="A. thaliana, Ohio State clone setced clones
/note="cDNA library was made from selected clones
Arabidopsis thaliana Ohio State clone set."
163 c 115 g 128 t
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/mol_type="mRNA"
/db_xref="taxon:3702"
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94.7%;
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Pred. No. 6.4e+02;
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rain CBS 94 of
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AUTHORS
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BF129496
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KEYWORDS
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                                                                                                                          Bource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  818 AAAAACGACAATGACCACA 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: sequefagenoscope.cns.fr - Web : This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
                                                                                                                                           found through the I.M.A.G.E. Consortium/LLNL at: http://image.lnl.gov
Plate: LLCM893 row: n column: 16
High quality sequence start: 132
High quality sequence stop: 163.
Location/Qualifiers
                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 1752)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               601811063R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4054095 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BF129496.1 GI:10968446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           343
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                    /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4054095"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="end :
                                                                       organism="Homo sapiens"
|mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:5482"
/clone="BDOAA010C06"
/clone_lib="BDOAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Candida tropicalis"
|mol_type="genomic DNA"
|strain="CBS 94"
tissue_type="primary B-cells from tonsils (cell line)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87.0%;
94.7%;
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Pred. No. 8e+02;
0; Mismatches
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RESULT 6
BY030666/c
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                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                 Nikaido, I., Osato, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schombach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Goyobori, T., Baldarelli, R., Hill, D. P., Bult, C., Corbini, L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C.F., Forrest, A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Pertea, G., Percovsky, N., Pillai, R., Pontius, J. U., Oi, D., Ramachandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B.Z., Kangaidin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K., Suttana, R., Takenaka, Y., Taylor, M. S., Teasdalle, R. D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Wattana, R., Takenaka, Y., Taylor, M. S., Teasdalle, R. D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Wattana, R., Takenaka, Y., Taylor, M. S., Teasdalle, M., Yang, L., Yang, L., Zavolan, M., Zhu, Y., Zimmer, A., M., Yang, L., Xang, L., Wang, Z., Zavolan, M., Zhu, Y., Zimmer, A., M., Yang, E., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Kyana, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shibata, Y., Index, J., Barney, E. and Hayashizaki, Y., Lander, S., Shibata, T., Sanglis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            251 AAAACGCCAATGGCCACAG 269
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Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
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//clone_Toygan: B-cells; Vector: pOTB7; Site_1: XhoI;
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
/note="Organ: B-cells; Vector: pOTB7; Site_sis_tells;
Directionally cloned into EcoRI/XhoI sites using the following 5; adaptor: GGCACGAG(G). Size_selected >500bp for average insert size 1.8kb .Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH MGC Library."

68 a 455 c 497 g 331 t 1 others
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'clone_lib="NIH_MGC_48"
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Pred. No. 9.9e+02;
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          230-0045, Japan
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AI395866
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
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URL:http://genome.gsc.riken.go.jp/
Alzawa,K. Akimura,T. Arakawa,T. Carninci,P., Fukuda,S., Hirozar
Alzawa,K. Jahii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,J.
T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Myazaki,J.,
Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,
Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami
Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami
M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
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Please visit our web site (http://genome.gsc.riken.go.jp) for
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AI395866.1 GI:4225413
EST.
Schistosoma mansoni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MA000059b.FGR Adult worm cDNA e mansoni cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                            Schistosoma
Tel: 55 31 2953566
Fax: 55 31 2952115
Email: oliveira@netra.cpqrr.fiocruz.br
                                                                                                                                                                                                                                                     Oliveira, G.C.
                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma
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                                                                                                                                                                                                                             Cataloguing Schistosoma mansoni genes with
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htro de Pesquisas Rene Rachou -
Augusto de Lima 1715 Barro Pro
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/dev stage="1 cell embryo"
/clone lib="RIKEN full-length enriched,
83 c 126 g 111 t
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="I0C0014E12"
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w Sakai,K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: szhao@tigr.org
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are derived from the mouse BAC library availability, please contact Pieter de Jong
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bapac.med.buffalo.edu/orderingframe.htm)
BACPAC Resources (http://bapac.gend.om). BAC end page:
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
plate: 422 row: G column: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhao, S., Nierman, W., Feldblyum, T.,
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Mouse BAC End Sequences from Library RPCI-23
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1 (bases 1 to 179)
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Mammalia; Eutheria; Rodentia;
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Class: BAC ends
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/strain="LE"
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/clone_lib="RPCI-23"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
ECORI; Site_2: ECORI; Female C57BL/6J mouse kidney and
brain genomic DNA was isolated and partially digeste
                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                         db xref="taxon:10090"
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90.0%;
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Pred. No. 8.5e+02;
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Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Malek, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MD 20850, USA
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VERSION
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AQ106085/c
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                                                                                                                                   BASE COUNT
ORIGIN
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Best Local Similarity
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74
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 241)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
                                                                                                                                                                                                                                                                                                                                                         Plate: 3054 ro
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                       Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
                                                                                                                                                                                                                                                                                                                                                                                                                                            401 Queen Anne Avenue North, Tel: (206) 616-3618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High Throughput Sequencing Center 
University of Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Mahairas GG, Wallace JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 scanning the human genome Proc. Natl. Acad. Sci. U.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10449764
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
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AGAAACGCCAATGAACACAG 55
                        AAAAACGCCAATGACCACAG
                                                                                                                                                                                                                                                                                                                     quality sequence stop: 241.
Location/Qualifiers
                                                                 Conservative
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                                                                                                                                             /clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: Sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH108"
1 54 c 52 g 83 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). "BH10B electrocompetent cells (BRL Life Technologies)."
                                                                                                                                                                                                                                                       /mol_type="genomic DN
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                     organism="Homo sapiens"
                                                                                                                                                                                                                                    clone="Plate=3054 Col=23 Row=I"
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90.0%;
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Pred. No. 8.6e+02;
                                                                               Score 16.8;
Pred. No. 9.
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RESULT 10 BZ664659/c

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RESULT 11
BE239439/c
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Best Local
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BE239439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18;
                                                                                 Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
. eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H.,,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Zimmerman,J. and Ecker,J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BZ664659
321 bp DNA linear GSS SALK 099680.45.60.x Arabidopsis thaliana TDNA insertion Arabidopsis thaliana genomic clone SALK 099680.45.60.x,
Harrison,M.J., Town,C.D., Bow
Holt,I.E., Cho,J. and Fraser,
ESTs from phosphate-starved r
                                                                                                                                                                                                                                                                                       EST392780 MHRP- Medicago
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Spermatophyta; Magnoliophyta; eudicotyledons; core eud: eurosids II; Brassicales; Brassicaceae; Arabidopsis. [ (bases 1 to 321)
                                                                                                                                                                                                                           BE239439.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At2g23500.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 858 453 4100 x1752 Fax: 858 558 6379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A Sequence-Indexed Library of Insertion Mutations in the
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                                                                                                                                                                                    Medicago truncatula (barrel medic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: ecker@salk.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis Genome
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                                                            (bases 1 to 393)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Ārabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
a 40 c 86 g 104 t
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/mol_type="genomic DNA"
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90.0%;
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Pred. No. 1.1e+03;
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                                                                                                                                                                                                                                                                                            truncatula cDNA clone
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                   Bowman, C.L.,
ser, C.M.
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  of.
                                                                                                                                                                                                                                                                                                               mRNA
Medicago truncatula
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                                      Craven, M.B., Hansen, T.S.,
                                                                                                                                                                                                                                                                                                               linear
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Prednis, L
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RESULT 12
AQ432032
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PUBMED
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424 bp DNA linear GSS 31-MAR-199
HS 2270 A2 E11 T7C CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=2270 Col=22 Row=I, genomic survey
               Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
                                                                                                      Sequence-tagged connectors: A sequence approach to mapping scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 424)

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Mahairas,G.G., Wallace,J.C., Young,J., Zhao,S., Adams,M.D. au
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             μ
University of Washington
                                                                                       99380589
                                                                                                                                                                                                                                                                                                    Homo sapiens
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The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73401, USA
Tel: 580-223-5810
                                                                                                                                                                                                                                                                                                                          Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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Seq primer: SKmod (CTA gAA CTA g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The Samuel Noble Roberts Foundation: N260974e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mjharrison@noble.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
Contact: Maria J. Harrison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAAAACGCCAATTGCCACAG 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAAACGCCAATGACCACAG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence name:MTHAU82TK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note=Wector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; At the trifoliate stage, M. truncatula plants were transplanted to phosphate-free sand and grown for a further 30 days. During this period, they were fertilized twice weekly with 1/2 Hoaglands solutions containing 20um potassium phosphate. cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using CJNA inserts were excised from the recombinant lambda-Zap cDNA inserts were excised from the recombinant lambda-Zap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                phage using Ex-assist helper phage and propagated in
XLOLR cells."
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/lab_host="XLOLR"
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/cultivar="A17"
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90.0%;
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Pred. No. 1.1e+03;
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AI735704/c
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Best Local S
Matches 18
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1 (bases 1 to 436)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                          High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (infc@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                              Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AI735704 436 bp mRNA linear EST 14-JUN-199
at20d01.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone
IMAGE:2355649 3' similar to gb:MSB458 40S RIBOSOMAL PROTEIN S4, X
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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Location/Qualifiers
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                                                                                                                                     /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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'clone_lib="Barstead aorta нгыкво
'note="Organ: aorta; Vector: pT7T3D-Pac (Pharmacia) with
                                                    /dev_stage="adult, age 64"
/lab_host="DH10B (phage resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="plate=2270 Col=22 Row=I"
                                                                                                     'sex="male'
                                                                                                                      clone="IMAGE: 2355649"
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Organ: sperm; Vector: pBeloBAC11; BAC Clones i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>,,</u>
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Pred. No. 1.
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AI243573/c
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208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 445)

NCI/NINDS-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological

Disorders and Stroke, Brain Tumor Genome Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
unknown library type
Trace considered overall poor quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AI243573
AI243573.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
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AAAAATGCCAATGACAACAG 189
                               AAAAACGCCAATGACCACAG 20
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                                                                                                                                      /clone lib="NCI CGAP Brn35"
/clone lib="NCI CGAP Brn35"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Sall;
/site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.33 kb. Tumor types include:
meningioma, oligodendroglioma, astrocytoma (grade II),
medulloblastoma, astrocytoma (grade IV). Life Technologies
catalog #: 11544-012"
a 85 c 92 g 162 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barstead.
                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1976746"
                                                                                                                                                                                                                                                                                     /tissue_type="tumor, 5 pooled (see description)"
/lab_host="DH108"
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This_clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               800 bp mRNA lines ut66h01.x1 Soares mouse NMGB bcell Mus musculus IMAGE:3332976 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 480.
Location/Qualifiers
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MGI:1077140
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National Cancer Institute, Cancer Genome Anat
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                 Conservative
                                                                                                                                             T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized; constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                               /mo1_type="mRNA"
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